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(54) Title: MODULATING DEVELOPMENTAL PATHWAYS IN PLANTS

(57) Abstract: The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein.



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Title: Modulating developmental pathways in plants.

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The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain *et al.* 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt *et al.* 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

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Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5 Y14600|SBRLK1|*Sorghum bicolor*
BF004020|BF004020|EST432518 KV1 *Medicago truncatata*
AW934655|AW934655|EST353547 tomato
AW617954|AW617954|EST314028 *L. pennellii*
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
10 AA738545|AA738545|SbRLK3 *Sorghum bicolor*
BG595415|BG595415|EST494093 cSTS *Solanum tuberosa*
AI896277|AI896277|EST265720 tomato
BF643238|BF643238|NF002H05EC1F1045
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
15 BE658174|BE658174|GM700005A20D5 Gm-r1070 *Glycine max*
BF520845|BF520845|EST458318 DSIL *Medicago truncata*
AC069324|AC069324|*Oryza sativa*
AW761055|AW761055|sl70d06.y1 Gm-cl027 *Glycine max*
BE352622|BE352622|WHE0425_G11_M21ZS Wheat
20 BG647340|BG647340|EST508959 HOGA *Medicago truncata*
AY028699|AY028699|*Brassica napus*
AW666082|AW666082|sk31h04.y1 Gm-cl028 *Glycine max*
AA738547|AA738547|SbRLK5 *Sorghum bicolor*
BG127658|BG127658|EST473220 tomato
25 L27821|RICPRKI|*Oryza sativa*
BG238468|BG238468|sab51a09.y1 Gm-cl043 *Glycine max*
BG441204|BG441204|GA_Ea0012C15f *Gossypium arbo.*
AW667985|AW667985|GA_Ea0012C15 *Gossypium arbore.*
AW233982|AW233982|sf32g05.y1 Gm-cl028 *Glycine max*
30 AP003235|AP003235|*Oryza sativa*
BF460294|BF460294|074A05 Mature tuber
AY007545|AY007545|*Brassica napus*
AC087544|AC087544|*Oryza sativa*
AB041503|AB041503|*Populus nigra*

35

The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the
40 Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.
 However, they lack a transmembrane domain while they do
 contain a signaling sequence at the N-terminal end. Therefore
 these proteins are thought to be positioned within vesicles
 5 within the plant cell or at the outside of the plasma
 membrane, within the cell wall of the plant cell. A number of
 homologs have been detected in other plant species, such as:

- AF370543|AF370543|*Arabidopsis thaliana*
 10 AF324989|AF324989|*Arabidopsis thaliana*
AV520367|AV520367|*Arabidopsis thaliana*
AV553051|AV553051|*Arabidopsis thaliana*
BF642233|BF642233|NF050C09IN1F1069
AW559436|AW559436|EST314484 *DSIR Medicago truncata*
 15 BG456991|BG456991|NF099F02PL1F1025
AW622146|AW622146|EST312944 tomato
BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*
BE322325|BE322325|NF022E12IN1F1088
BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*
 20 BE460627|BE460627|EST412046 tomato
BI204894|BI204894|EST522934 *cTOS Lycopersicon esculentum*
BI205306|BI205306|EST523346 *cTOS Lycopersicon esculentum*
BI204366|BI204366|EST522406 *cTOS Lycopersicon esculentum*
AW443205|AW443205|EST308135 tomato
 25 AW031110|AW031110|EST274417 tomato
BI180080|BI180080|EST521025 *cSTE Solanum tuberosa*
BF644761|BF644761|NF015A11EC1F1084
AV526127|AV526127|*Arabidopsis thaliana*
AV556193|AV556193|*Arabidopsis thaliana*
 30 BE203316|BE203316|EST403338 *KV1 Medicago truncatata*.
AW649615|AW649615|EST328069 tomato
BE512465|BE512465|946071E06
BI204917|BI204917|EST522957 *cTOS Lycopersicon esculentum*
BG590749|BG590749|EST498591
 35 BG648725|BG648725|EST510344 *HOGA Medicago truncata*
BG648619|BG648619|EST510238 *HOGA Medicago truncata*
BG597757|BG597757|EST496435 *cSTS Solanum tuberosa*
AW221939|AW221939|EST298750 tomato
BE704836|BE704836|Sc01_
 40 BG124409|BG124409|EST470055 tomato

- BF051954 | BF051954 | EST437120 tomato
BG320355 | BG320355 | Zm03_05h01_Zea mays
AV526624 | AV526624 | Arabidopsis thaliana
AW933960 | AW933960 | EST359803 tomato
5 AW221278 | AW221278 | EST297747 tomato
BE405514 | BE405514 | WHE1212_C01_F02ZS Wheat
BG314461 | BG314461 | WHE2495_A12_A23ZS Triticum
BF258673 | BF258673 | HVSMEf0016G01f *Hordeum vulgare*
BG262637 | BG262637 | WHE0938_E03_I06ZS Wheat
10 AW030188 | AW030188 | EST273443 tomato
BG653580 | BG653580 | sad76b11.y1 Gm-cl051 *Glycine max*
BG319729 | BG319729 | Zm03_05h01_A Zm03_ *Zea mays*
BF053590 | BF053590 | EST438820 potato
BE454808 | BE454808 | HVSMEh0095C03f *Hordeum vulgare*
15 BI075801 | BI075801 | IP1_21_D05.b1_A002
BE367593 | BE367593 | PI1_9_F02.b1_A002 *Sorghum bicolor*
2e-074 BF260080 | BF260080 | HVSMEf0021A22f *Hordeum vulgare*
BF627921 | BF627921 | HVSMEb0006I23f *Hordeum vulgare*
BG598491 | BG598491 | EST503391 cSTS *Solanum tuberosa*
20 AW038168 | AW038168 | EST279825 tomato
BG343258 | BG343258 | HVSMEg0005D23f *Hordeum vulgare*
AW925684 | AW925684 | HVSMEg0005D23 *Hordeum vulgare*
BG416093 | BG416093 | HVSMEk0009L18f *Hordeum vulgare*
AW683370 | AW683370 | NF011C09LF1F1069
25 BE420108 | BE420108 | WWS020.C1R000101 ITEC WWS Wheat
AW350720 | AW350720 | GM210009A10F4 Gm-r1021 *Glycine max*
AW616564 | AW616564 | EST322975 L. *Hirsutum trichome*
AW011134 | AW011134 | ST17B03 Pine
BF630746 | BF630746 | HVSMEb0013N06f *Hordeum vulgare*
30 AW926045 | AW926045 | HVSMEg0006C10 *Hordeum vulgare*
BE519800 | BE519800 | HV_CEb0021E12f *Hordeum vulgare*
BG343657 | BG343657 | HVSMEg0006C10f *Hordeum vulgare*
BG933682 | BG933682 | OV1_16_C09.b1_A002
BE433368 | BE433368 | EST399897 tomato
35 AW219797 | AW219797 | EST302279 tomato
BF629324 | BF629324 | HVSMEb0010N06f *Hordeum vulgare*
BE597128 | BE597128 | PI1_71_A07.g1_A002
AW220075 | AW220075 | EST302558 tomato
AW616639 | AW616639 | EST323050 L. *Hirsutum trichome*
40 BF645214 | BF645214 | NF032F11EC1F1094
AW924540 | AW924540 | WS1_70_H12.b1_A002

- AI775448|AI775448|EST256548 tomato
AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*
BF270171|BF270171|GA_Eb0007B13f *Gossypium arbor.*
BE919631|BE919631|EST423400 potato
5 AW037836|AW037836|EST279465 tomato
BF008781|BF008781|ss79h09.y1 Gm-cl064 *Glycine max*
BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*
BE599797|BE599797|PI1_79_H01.g1_A002
BE599026|BE599026|PI1_86_E03.g1_A002
10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*
BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*
AW307218|AW307218|sf54c07.y1 Gm-cl009 *Glycine max*
AI496325|AI496325|sb05c09.y1 Gm-cl004 *Glycine max*
AJ277703|ZMA277703|*Zea mays*
15 AL375586|CNS0616P|*Medicago truncatula* EST
AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*
BE125918|BE125918|DG1_59_F02.b1_A002
BF053901|BF053901|EST439131 potato
BE921389|BE921389|EST425266 potato
20 BE597551|BE597551|PI1_71_A07.b1_
BE360092|BE360092|DG1_61_C09.b1_A002
BE660084|BE660084|491 GmaxSC *Glycine max*
AJ277702|ZMA277702|*Zea mays*
- 25 The invention also relates to modifying SBP/SPL gene or
products which represent a family of transcription factors
with a bipartite nuclear localization signal (The SQUAMOSA
PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of
Arabidopsis thaliana, Columbia ecotype). Upon activation
30 (probably by RKS mediated phosphorylation, the bipartite
nuclear localization signal becomes linear and available for
the nuclear translocation of the protein. Within the plant
nucleus, the transcription factor regulates transcription by
interaction with specific promoter elements. .In *Arabidopsis*
35 *thaliana*, this family is represented by at least 16 different
members (see following list). In many other plant species, we
also identified members of this transcription factor family
(See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: <http://www.ub.uni-koeln.de/ediss/archiv/2001/11w1204.pdf>; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

20

	name	genetic code
	ATSPL1	At2g47070*
	ATSPL2	At5g43270
	ATSPL3	At2g33810*
25	ATSPL4	At1g53160*
	ATSPL5	At3g15270
	ATSPL6	At1g69170
	ATSPL7	At5g18830
	ATSPL8	At1g02065
30	ATSPL9	At2g42200*
	ATSPL10	At1g27370*
	ATSPL11	At1g27360*
	ATSPL12	At3g60030
	ATSPL13	At5g50570
35	ATSPL14	At1g20980
	ATSPL15	At3g57920
	ATSPL16	At1g76580

* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5 AB023037|AB023037|*Arabidopsis thaliana*
BG789832|BG789832|sae56b07.y1 Gm-cl051 *Glycine max*
BG123992|BG123992|EST469638 tomato
BG595750|BG595750|EST494428 cSTS *Solanum tuberosum*
AF370612|AF370612|*Arabidopsis thaliana*
- 10 BF728335|BF728335|1000060H02.x1 1000 - *Zea mays*
X92079|AMSBP2|*A.majus*
AW331087|AW331087|707047A12.x1 707 - Mixed adult... 128 *zea mays*
AJ011643|ATH011643|*Arabidopsis thaliana*
L34039|RICRMSOA|*Oryza sativa*
- 15 AJ011638|ATH011638|*Arabidopsis thaliana*
AJ011639|ATH011639|*Arabidopsis thaliana*
AJ132096|ATH132096|*Arabidopsis thaliana*
BF482644|BF482644|WHE2301-2304_A21_A21ZS Wheat
BF202242|BF202242|WHE0984_D01_G02ZS Wheat
- 20 BE057470|BE057470|sm58e10.y1 Gm-cl028 *Glycine max*
AJ011628|ATH011628|*Arabidopsis thaliana*
AJ011629|ATH011629|*Arabidopsis thaliana*
AJ011617|ZMA011617|*Zea mays*
AJ011637|ATH011637|*Arabidopsis thaliana*
- 25 AJ011622|AMA011622|*Antirrhinum majus*
AJ011621|AMA011621|*Antirrhinum majus*
AJ011635|ATH011635|*Arabidopsis thaliana*
AJ011623|AMA011623|*Antirrhinum majus*
BF650908|BF650908|NF098D09EC1F1076
- 30 AJ242959|ATH242959|*Arabidopsis thaliana*
Y09427|ATSPL3|*A. thaliana* mRNA
AJ011633|ATH011633|*Arabidopsis thaliana*
AW691786|AW691786|NF044B06ST1F1000
BE058432|BE058432|sn16a06.y1 Gm-cl016 *Glycine max*
- 35 AW728623|AW728623|GA__Ea0017G06 *Gossypium arbore.*
BG442540|BG442540|GA__Ea0017G06f *Gossypium arbo.*
AJ011626|ATH011626|*Arabidopsis thaliana*
AJ011625|ATH011625|*Arabidopsis thaliana*
AI993858|AI993858|701515182 *A. thaliana*
- 40 BG593787|BG593787|EST492465 cSTS *Solanum tuberosum*
BF634536|BF634536|NF060C08DT1F1065 Drought *Medicago*

- BE806499|BE806499|ss59f10.y1 Gm-c1062 *Glycine max*
AW933950|AW933950|EST359793 tomato
AC008262|AC008262| *Arabidopsis*
B28493|B28493|T10A24TF TAMU *Arabidopsis thaliana*
- 5 AJ011644|ATH011644|*Arabidopsis thaliana*
AC018364|AC018364|*Arabidopsis thaliana*
AL092429|CNS00VLB|*Arabidopsis thaliana*
BE435668|BE435668|EST406746 tomato
BG097153|BG097153|EST461672 potato
- 10 BE440574|BE440574|sp47b09.y1 Gm-c1043 *Glycine max*
AI443033|AI443033|sa31a08.y1 Gm-c1004 *Glycine max*
U89496|ZMU89496|*Zea mays* liguleless1
AW433271|AW433271|sh54g07.y1 Gm-c1015 *Glycine max*
AW932595|AW932595|EST358438 tomato
- 15 AW096676|AW096676|EST289856 tomato
AJ011616|ZMA011616|*Zea mays*
AW036750|AW036750|EST252139 tomato
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*
AJ011614|ZMA011614|*Zea mays*
- 20 AJ011642|ATH011642|*Arabidopsis thaliana*
BE022435|BE022435|sm85h04.y1 Gm-c1015 *Glycine max*
X92369|AMSPB1|*A.majus*
AC015450|AC015450|*Arabidopsis thaliana*
AC079692|AC079692|*Arabidopsis thaliana*
- 25 AJ011632|ATH011632|*Arabidopsis thaliana*
AJ011631|ATH011631|*Arabidopsis thaliana*
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*
AJ242960|ATH242960|*Arabidopsis thaliana*
AJ011610|ATH011610|*Arabidopsis thaliana*
- 30 AJ132097|ATH132097|*Arabidopsis thaliana*
AL138658|ATT209|*Arabidopsis thaliana*
AJ011615|ZMA011615|*Zea mays*
BE499739|BE499739|WHE0975_ Wheat
AW398794|AW398794|EST309294 *L. pennellii*
- 35 AJ011618|ZMA011618|*Zea mays*
AW747167|AW747167|WS1_66_F11.b1_
AJ011577|ATH011577|*Arabidopsis thaliana*
AI992727|AI992727|701493410 *A. thaliana*
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*
- 40 BE804992|BE804992|ss34h10.y1 Gm-c1061 *Glycine max*
BE325341|BE325341|NF120H09ST1F1009

- AC007369|AC007369|*Arabidopsis thaliana*
AJ011619|ZMA011619|*Zea mays*
BI099345|BI099345|IP1_37_H10.b1_A002
BI071295|BI071295|C054P79U *Populus*
5 AZ920400|AZ920400|1006019G01.y2 1006 -
AZ919034|AZ919034|1006013G02.x3 1006 -
BE805023|BE805023|ss35d09.y1 Gm-c1061 *Glycine max*
BG582086|BG582086|EST483824 GVN *Medicago truncata*
AJ011609|ATH011609|*Arabidopsis thaliana*
10 BE023083|BE023083|sm90e08.y1 Gm-c1015 *Glycine max*

- Furthermore, the invention relates to modifying NDR-NHL-genes
or gene products. All proteins belonging to this family
contain one (and sometimes even more than one) transmembrane
15 domain. *Arabidopsis* contains a large number of NDR-NHL genes,
such as:
aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),
aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,
aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, all63812,
20 f20d21-35, t13m11-12, fle22-7, t23g18, f5d14-4266, t32f12-16, f11f19-
11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043,
k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-
80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-
9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 ,
25 mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 ,
At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 ,
At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080
f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 ,
At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160
30 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 ,
At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600
K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450
F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 ,
At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860
35 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4123 , At4g30650 ,
At1g69500 F10D13

and

- 40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,
 At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,
 At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,
 At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,
 5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,
 NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,
 At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,
 At4g26820

10 NDR-NHL genes belong to a large family of which one of the
 first identified is the defence-associated gene HIN1 (Harpin-
 induced gene). HIN1 is transcriptionally induced by harpins
 and bacteria, that elicit hypersensitive responses in tobacco.
 It is thus believed that the genes of the invention also play
 15 arole in the hypersensitive reaction. Especially (see also
 chapter 8) since the genes of the invention bear relation to
 brassinoid-like responses and since brassinoid pathway
 compounds have been found to interact in this same defence
 system in plants. Other plant species also contain members of
 20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

25 BG582276|BG582276|EST484016 GVN *Medicago truncata*
AV553539|AV553539|*Arabidopsis thaliana*
AC069325|AC069325|*Arabidopsis thaliana*
AV526693|AV526693|*Arabidopsis thaliana*
BG583456|BG583456|EST485208 GVN *Medicago truncata*
 30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*
BE997791|BE997791|EST429514 GVSN *Medicago truncata*
BG580928|BG580928|EST482657 GVN *Medicago truncata*
BF520916|BF520916|EST458389 DSIL *Medicago truncata*
AV544651|AV544651|*Arabidopsis thaliana*
 35 AV543762|AV543762|*Arabidopsis thaliana*
AW559665|AW559665|EST314777 DSIR *Medicago truncata*
BG581012|BG581012|EST482741 GVN *Medicago truncata*
AV552164|AV552164|*Arabidopsis thaliana*
BE999881|BE999881|EST431604 GVSN *Medicago truncata*
 40 AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*
AW219286|AW219286|EST301768 tomato
BE124562|BE124562|EST393597 *GVN Medicago truncata*
AV540371|AV540371|*Arabidopsis thaliana*
5 AV539549|AV539549|*Arabidopsis thaliana*
BG647432|BG647432|EST509051 *HOGA Medicago truncata*
BE434210|BE434210|EST405288 tomato
BG725849|BG725849|sae42g02.y1 Gm-cl051 *Glycine max*
AP003247|AP003247|*Oryza sativa*
10 BE348073|BE348073|sp11a11.y1 Gm-cl042 *Glycine max*
AW508383|AW508383|si40c06.y1 Gm-r1030 *Glycine max*
AI856504|AI856504|sb40b07.y1 Gm-cl014 *Glycine max*
BE556317|BE556317|sq01b07.y1 Gm-cl045 *Glycine max*
AA713120|AA713120|32681 *Arabidopsis*
15 AV541531|AV541531|*Arabidopsis thaliana*
AI894456|AI894456|EST263911 tomato
AW704493|AW704493|sk53g11.y1 Gm-cl019 *Glycine max*
AW219298|AW219298|EST301780 tomato
BF425685|BF425685|ss03c11.y1 Gm-cl047 *Glycine max*
20 AV422557|AV422557|*Lotus japonicus*
BE190816|BE190816|sn79a08.y1 Gm-cl038 *Glycine max*
BG580331|BG580331|EST482056 *GVN Medicago truncata*
AV423251|AV423251|*Lotus japonicus*
AI896088|AI896088|EST265531 tomato
25 AV413427|AV413427|*Lotus japonicus*
AV426656|AV426656|*Lotus japonicus*
AV416256|AV416256|*Lotus japonicus*
AL385732|CNS0690I|*Medicago truncatula*
AB016877|AB016877|*Arabidopsis thaliana*
30 AV419449|AV419449|*Lotus japonicus*
AI486269|AI486269|EST244590 tomato
AV411690|AV411690|*Lotus japonicus*
AV419925|AV419925|*Lotus japonicus*
AV418222|AV418222|*Lotus japonicus*
35 AV409427|AV409427|*Lotus japonicus*
AC005287|AC005287|*Arabidopsis thaliana*
AV426716|AV426716|*Lotus japonicus*
AV411791|AV411791|*Lotus japonicus*
BG351730|BG351730|131E12 Mature tuber
40 BG046452|BG046452|saa54b12.y1 Gm-cl060 *Glycine max*
AI781777|AI781777|EST262656 tomato

- BE451428|BE451428|EST402316 tomato
AI772944|AI772944|EST254044 tomato
AI895510|AI895510|EST264953 tomato
AW030762|AW030762|EST274017 tomato
5 AW218859|AW218859|EST301341 tomato
BE203936|BE203936|EST396612 *KV0 Medicago truncata*
AV410289|AV410289|*Lotus japonicus*
AW032019|AW032019|EST275473 tomato
AW030868|AW030868|EST274158 tomato
10 AV421824|AV421824|*Lotus japonicus*
BG646408|BG646408|EST508027 *HOGA Medicago truncata*
AF325013|AF325013|*Arabidopsis thaliana*
AC007234|AC007234|*Arabidopsis thaliana*
AW217237|AW217237|EST295951 tomato
15 AC034257|AC034257|*Arabidopsis thaliana*
AW625608|AW625608|EST319515 tomato
AW031064|AW031064|EST274371 tomato
AF370332|AF370332|*Arabidopsis thaliana*
AB006700|AB006700|*Arabidopsis thaliana*
20 AW035467|AW035467|EST281205 tomato
AL163812|ATF14F18|*Arabidopsis thaliana*
AI896652|AI896652|EST266095 tomato
AI730803|AI730803|BNLGH17970 Cotton
AW034775|AW034775|EST278811 tomato

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- The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex) comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling
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complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products
5 are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore
10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing
15 complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane
20 towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of
25 such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the
30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes
35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying

- 5 teh brassinosteroid pathway can, amongst others, be found in:
Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-
713, genetic evidence for an essential role of
brassinosteroids in plant development; J. Cell Biochem Suppl.
21a 479 (1995) ; Mandava 1988 Plant growth-promoting
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol.
39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-
182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66;
Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol.
Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory,
that modification of the RKS genes will result in a
modification of the brassinosteroid pathway, thereby giving
the various phenotypes that are shown below.

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"Functionally equivalent" as used herein is not only used
to identify the functional equivalence of otherwise not so
homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL
proteins, but also means an equivalent gene or gene product of
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in
Arabidopsis Thaliana, e.g. identifying a homologue found in
nature in other plants or a homologue comprising a deliberate
nucleic acid modification, such as a deletion, truncation,
insertion, or deliberate codon substitution which may be made on
30 the basis of similarity in polarity, charge, solubility,
hydrophobicity, and/or the amphipathic nature of the residues as
long as the biological activity of the polypeptide is retained.
Homology is generally over at least 50% of the full-length of
the relevant sequence shown herein. As is well-understood,
35 homology at the amino acid level is generally in terms of
amino acid similarity or identity. Similarity allows for
"conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,

5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant
10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery
20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides
25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and
30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an
35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

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In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*.

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Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

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regeneration capacity of in vitro cultured *Arabidopsis* callus. Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem.

Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more

introduced gene products interfere with normal pollen initiation and development is therefore highly desired.

Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR
NHL family

5 NHL10= At2g35980

maaeqplnga fygpsvpppa pkggyrrghg rgcgccllsl fvkviisliv ilgvaalifw
livrpraikf hvtdasltrf dhtspdnir ynlaaltvpvr npnkriglyy drieahayye
gkrfstittlt pfyqghkntt vltptfqgqn lvifnagqsr tlnerisgv ynieikfrlr
vrfklgdlkf rrikpkvdc dlrplstsn gttttstvf ikcdfdf

10

Atlg32270 syntaxin,

MVRSNDVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNQ
RLGAVPMP LF YLGSKNTMLL RALFEGQTLV LLKGNERRKF EDDQKTGVYR IDVKLSINFR
VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKKMLLI GQLVKDTSAN LREASETDHR
15 RDVAQSKKIA DAKLAKDFEA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS
QEQRVLMESR RQEIIVLLDNE ISLNEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHQQ
TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSLLFSC SLLLFFFLSG DLRCRCVCGS
ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK*

20

Below the homology is shown between NHL10 (Upper line) and a
syntaxin protein. (bottom line). The identical amino acids are
shown in the middle line.

25

IVRPRAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPNKRIGLYYDRIEAAHAYYEG
VR KF V DA LT FD S N L Y L L RN IG YDR EA YY
MVRSNDVKFQVYDAELTHFDLESNN-LQYSLSLNLSIRNSKSSIGIHYDRFEATVYYMN

30

KRFSTITLTPFYQGHKNTTVLTPTFQGNLVIFNAGQSRTLNAERISGVYNIEIKFRLRV
R FY G KNT L F GQ LV G V Y I K
QRLGAVPMP LF YLGSKNTMLL RALFEGQTLV LLKGNERRKF EDDQKTGVYR IDVKLSINF

35

RFKLGD LKFRR IKPKVDCDDLRLPLSTSN GTTT
R L KP V C L PL T
RVMVLHLVTWPMKPVRCH-LKIPLALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

http://mips.gsf.de/proj/thal/db/search/search_frame.html

5 searching for homologous sequences with the sequence At1g32270

gene code:

predicted function:

	At1g32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein	Syntaxin
	AtVam3p (gb AAC49823.1)	
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	At1g65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein	Syntaxin
	AtSNAP33	
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	At1g61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	At1g61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	At1g54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1g11250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5g42860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin
35		

40 This observation provides the explanation for understanding
the mechanism by which the RKS / NDR-NHL complex functions.
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

5 Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and
10 allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible as a monomer or a (hetero)dimerizing molecule binds the
15 transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.

One class of ligands interacting with the RKS and / or ELS
20 receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5' - towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'- and trailer sequences 3'-) are indicated in small letters.

Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence

The second (set of) lines represents the pro-peptide.

The last line represents the conserved Cysteine motif.

A. At1g22690

```

1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat
61 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacata tcattaagac
121 ataaactacc aaagtatcaa gctaattgtaa aaattactct catttccacg taacaaattg
181 agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcac
241 ctccgaaaaa aggyaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca
301 aatgcaatct ataactctgt atttatccaa taaaaacctg tgatttatgt ttggctccag
361 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa
421 gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc
481 aaaatcacta ctcaagaaat ATGAAGAAGA TGAATGTGGT GGCTTTTGTT ACGCTGATCA
541 TCTCTTTTCT TCTGCTTTCT CAGgtaaact gttaaaacca ttttcaagac taccttttct
601 ctattttcaga caaaccaaag taaaacaatg aaaaatctct ctggctcttc atagGTACTT
661 GCAGAGTTGT CATCATCCAG CAACAATGAA ACTTCCTCTG TTTCTCAGgt aagagtgata
721 caaaaacata ctaaacaaac tttcaagaga gtaatatata aggaaatggt ggcttctttt
781 ttttggttgc aatcagACGA ATGACGAGAA CCAACTGCG GCGTTTAAGA GAACATACCA
841 CCATCGTCCA AGAATCAgtt agtctactct ttcaacactc taattccttt gttctaagta
901 ttttttttgc cccccacaa ctttttttta ttaaatgagc caatttttat agATTGTGGG
961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTGTCA CAGAGCCTGT
1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CCGCCGGGAA CCTCCGGCAA CACAGCATCA
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1141 tctcatttct caactatagt ctcatcttct gattatgttt ctctctttgt tatgttgcat
1201 gtgtgatgtg tgagcttatt attatgttga ttgttgacat aattcaacta tataatttgt
1261 atcgattccg aataataaga tgagtgtatt tattggctat taagtttttt tttttttttt
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1381 agtttcatct tcatattaac acaaaatctc catacatatt accaaaccaa aaaaatacac
1441 aagggggaga gagaccaacg gttcttggtt cagagtttgc atcttgtttg agccgtcacc
1501 gtttcttaga cttaacagcc acaacacctt tataaagctt cagcgatcc ttcaacgcac
1561 ctgcgcgagg ccgagccacc ttattgtttg gatcaacaa caaaacttct tcaaacgcac
1621 tcaatgccaa aggc

```

MKKNVAVFTLIISFLLLSQVLA

ELSSSSNNETSSVSQTNDENQTAAFKRTYHHRPRIN

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B. At1g74670

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121 tttgtgttta tgtttgattt tacgttttta tatgtaaata agatatatta cgaattatgg
181 tttttatttg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat
241 aaagtaatat aatataatgta ccgttattaa ctattgttac atgtgaatga ggaagcttac
301 acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa
10 361 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc
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481 TCACTTTCGT TTGTCTCACT ATGTCAAAG AAGCTGAGTA CCATCCAGAA AGTgtaagtt
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15 601 tccctttcta tttattgcta taaatctaatt acccgcgta aaatttgttt tgaattataa
661 cagTATGGAC CAGGAAGTCT GAAATCATAC Cgtaagtaaa aacttcttct tcttttatga
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25 1261 attttacttt ctaagtttgt ataactatat cttaaaagtg ttagacagag tcctaattgat
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1441 tttcgacgat gat

30

MAKLITSFLLLTILFTFVCLTMS

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35

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C. At1g75750

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121 atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgat aaaatacaaa
181 tgattttctca attacctaaa aaatataaaa atgtcttact ttattttcag ccactgttgg
241 aaagtacttg caatcatatc gtattttgaa ttataaaaact cagaaacaat tattttccct
301 gaaaagttaa aacttttaat aagatattta taaaataaaa agaatagtct agaccgaaaa
10 361 tggggtcggt tgtccatcca aaggagtgtc ataaatagaa ccctccaagt tctcattagg
421 acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca
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841 CTGTGTCACA GAGCGTCCGG GACTTGCTGC TACAGGTGCA ACTGTGTGCC TCCGGGTACG
901 TACGGAAACT ACGACAAGTG CCAGTGCTAC GCTAGCCTCA CCACCCACGG TGGACGCCGC
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30

MAISKALIASLLISLLVLQLVQA

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35

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D. At2g14900

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35

MKIIVSILVLASLLLISSSLASATIS

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E. At2g18420

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F. At2g30810

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15 661 aatatcaatg ttatttttca aactacataa ttttaaaata ttttattgat aacacaaatg
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1561 tgctctatta aaaatgatta aataaataat aata

MMKLIVVFVISSLLFATQFSNG

35

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40

G. At2g39540

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541 TCCTCACATC TTCATTTTCT GTACTTTCAA GTGCTGATTC GTgtaagtgt ttacttaatc
601 tagttaataa ttgtaggtca tgcattgtatc attttgaaac aagtthttctg aaattcttaag
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1261 thtttgagaga thcgtthact cactaccgga gaacgacgct atgtcagaga ccgccgtgtc
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MKLVVVQFFIISLLLTSSFSVLSSA

30

DSS

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35

H. At3g02885 (GASA5)

5 1 cgcttttctat tacactttttt tttctttttta gtcgcacttc acaattagct taattaattt
61 cctaaaactcg cttatttttcc cttttctata tacagatatt atcatttagtg acatttttcat
121 tttccaaaaca gagcgttttag acactagtca actacacaat ataatttttcc aatttttccat
181 gagagaaatg tttttttttt ttttttccaa ggcaagattt tagtcttttg gttctctata
241 cgtgggtaat tagtgattag taattttacac tggtagtctt ttgacattgt ctaagagaca
10 301 aaaacgacaa gtgtggtacg taattagaaa ttaaaatgac ctacttcccc agaatcacgg
361 catgaacatt ggcaatacca aattttcttga ataccattga agysaatcca cactaatcat
421 tttctctata aatatcttta atccgtttta ttgtttctta agaatcattc attggcaatc
481 aagattttttt aacccaaaaaa ATGGCGAATT GTATCAGAAG AAATGCTCTT TTCTTCTTGA
541 CTCTTCTCTT TTTATTGTCA GTCTCCAACC TCGTTCAGgt aaaccactca aaacagattc
15 601 agtttatttaa agtctgatat tgaagtttta tataattacag gctgctcgtg gaggtaaaaa
661 tgaccaaaagg ctatacattc cttaaaaaatt taatggctat tagttttctg atattgaagt
721 tttatatata tatgacagGC TGCTCGTGGT GGTGGCAAAC TCAAACCCCA ACgtacggac
781 tcaaaaacttt tgttgtttca tatgatcata ttaattttatt aatcactaat tattgataat
841 gttgataaat aaacttttaaa gtaacaataa tgggtgtttat tttgtgaaat gtcagttttc
20 901 tagtatactg tatgtgtgtga attataagca tgaacataaa gatctcaatg atttgttttt
961 tgtttgtttg ttgtgatatg cttttttgat ggaaacttca attgttagAGT GCAACTCAAA
1021 GTGTAGCTTC CGTTGTTTCA CAACATCACA CAAGAAGCCA TGCAATGTTCT TTTGCCTCAA
1081 GTGTTGCAAA AAATGTCTTT GTGTCCTCC TGGCACTTTC GGCAACAAAC AAACCTGTCC
1141 ATGTTACAAC AACTGGAAGA CTAAAGAAGG CCGTCCAAAA TGTCCTTAAa acttcttttt
25 1201 agatatattt gataaatattc atctagtttt ggattatcaa acacttacta ctctgtttta
1261 atctgtttct acaagttggc gatttgtctc tacacttttt ttgtgtcttt tgctcttaac
1321 tgttgtgttt gttatacgtg taagcccgcc caatgtgtca tggccgaact tattatgggt
1381 acatattttat gaaatgggct tcattatcaa ttgatttgag cctacaaaaa tgtagccata
1441 aagcccatta agttgtaatt gttaatattt cagtcataaa tatgattttc tatatctatg
30 1501 atttatctct agtgttgatg atgtttgtat gtggaagtca tgttctattt gcttccacgg
1561 tttaaaaacc atcaacttgc taagggtcaaa ttctaataat actgtgaaaa acattattta
1621 cgtgcgtaat tatatgaatt tatgaatagg ttttaattcc attttttcct aatagtgttt
1681 tatgtcaaa

35

MANCIRRNALFFLTLLFLLSVSNLVQAA

40 RGGGKCLKPQQ

CNSKCSFRCSATSHKKPCMFFCLKCKKCLCVPPGTFGNKQTCPCYNNWKTKEGRPKCP*

45

I. At4g09600 (GASA3)

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5      1 taggctggca atttaactct gagacgtctt tcttgatat agaataaaac atacgcggtg
      61 aaaagaaaaac gcgtgaatcg aatgatgagt gttaacgttc gatcgagatg ccaccaaatc
     121 ttttcattaa aatgaattgt ggaggacata ccacttttaa cgaggtcatt tccactgggt
     181 gacatgtgga ctctactttg ggtggcatgt tcatatcttt ccacatcacc atgtaaacgt
     241 gaaaacaccc accacactca cttacatctc aaacacatgt cttcattatc gtacgtagct
     301 ccaaaaaaaa aaatgaaaaa taggtttagt gattctatct cgcaatgtat aatatacaac
    10 361 ttgtaaaaat aaaatatttg aataagcatt ataaataaac ccaagaggtt gtttagattta
     421 tatacttaat tgtagctact aaatagagaa tcagagagaa tagttttata tcttgcacga
     481 aactgcattgc tttttgagac ATGGCAATCT TCCGAAGTAC ACTAGTTTTA CTGCTGATCC
     541 TCTTCTGCCT CACCACTTTT GAGgttcata acttttgtct ttacttctcc atgaatcatt
     601 tgcttcgtct tatccttaat tcatatgtgt ttgatcaatg ataataattc atcattctct
    15 661 tcagCTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGAAAATTGg
     721 tatgtaacgc taacatatat gtaaagtgtt atatctctgt ttatatatga tttttaaacg
     781 gttaaaaaact agtcatatgt gtataaatat atcatgtgaa gATTGCGGTG GGAGATGCAA
     841 AGGTAGATGC AGCAAATCGT CGAGGCCAAA TCTGTGTTTG AGAGCATGCA ACAGCTGTTG
     901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAC CACCACCTTT GTCCTTGCTA
    20 961 CGCCTCCATT ACCACTCGTG GTGGCCGCTT CAAGTGCCCT TAAacatata cacatacaga
    1021 tgtgtgtata tgtcttccgc gagcacacac gtacgtttat gttttaagga caatagtatg
    1081 tatgagcagc tataaacaaa ccagaagtta atggttcatg ttgaactagt ataagttgta
    1141 tgaactgtgc ttcttttgaa caaccacttt tgctgtaagt ttagcaaccc tatttaataa
    1201 attagagatt acaaaaaaaa aaatgaaaaa tgtttaaaaa acgtggattt ttaaatattg
    25 1261 gattaaaaat taattttcat tttggttgat ttgtcaataa attagctaag ttttgtatac
    1321 tagggccgttt aagatatgct gttaaatttt tgataataga gttgccttag aagttcataa
    1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga
    1441 atcgaattga ccagaactga aagaaagtaa aagaaaagct gaatacagag aatttaacga

30  MAIFRSTIVLLLLILFCLTTF
    ELHVHAAEDSQVGEGVKID

35  CGGRCKGRCSKSSRPNLCLRACNSCCYRCNCVPPGTAGNHHLCPCYASITTRGGRLKCP*

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J. At4g09610 (GASA2)

5 1 ttaacagttt aacaccataa tgttaaactc ggttttagcat tttggtgtaa ttctacctct
61 ttaaccatac atactaaaga cgcagagaag ttcatatggt agttaatcgt aaatagctaa
121 acttttaatt ggggttaaca tattatttaa cacttaacat ttaactattg atctctcatt
181 ttttttttat taaccaaaat aaattcattt tagaaccaaa cgtttcaaaa actcgtaatg
241 tttcttcatt aaatcttate tatagctcac acaaagaaaa actacggaca tgcattgcacc
301 caattatata catggattat tttttttagt gttataatat gatacaaaaat aaaaaacatt
10 361 tggatagccg ataggcgata gccactataa atataccaaa gaggttggat tatacatata
421 gccgtaatac caaagagagt atcagataga aatagttcta atattttgta caactcacag
481 aaattgcatg agtttcgaac ATGGCAGTCT TCCGAAGTAC ACTGGTCTG TTAATAATCA
541 TCGTCTGTCT CACCACTTAT GAGgtttata atatttttgg tctttatagt tccccaagaa
15 601 cacttagcaa tattatactc aattcatggt tatatgataa tgactgatca ttctcttcag
661 CTTACAGTCC ACGCTGCTGA TGGTGCAAAG GTCGGTGAAG GCGTAGTGAA AATCGgtatg
721 taaccctaac ttatatataa cacgttggta tataacttaa tattctgatg gggtcgactc
781 tcttcccaac ttatatatat ctttgttatg gagaatgtct caagcttita atgagatggt
841 atatctcgga gaagyaact atgaactaaa agctttggat tcctttgcaa caaatataaaa
901 cttttgatgg gtttaaacgg attaaattag ttacatgtgt ttgatgaatg tatgtatgat
20 961 tgtagATTGT GGTGGGAGAT GCAAAGATAG ATGCAGCAA TCTTCGAGAA CGAAGCTATG
1021 CTTGAGAGCG TGCAACAGCT GTTGTCCCG CTGCAACTGT GTGCCACCTG GACTTCTGG
1081 AAACACCCAC CTTTGTCTT GCTACGCCTC CATTACCACT CACGGTGGCC GCCTCAAGTG
1141 CCTTAaAat ttcttctgtg tctgtttctg tttctacttc tatttcgaat atatgtacat
25 1201 gtgtgtgtac gtgtgtatgt atacaagtac tgctatgttt tggaggacaa aagtatatgt
1261 atgagaagct ataaactaat tagaagttga tggttatgctg tattatcaaa ccgtgttact
1321 tctgaacaac caatttcggt ttgttccaag tttggcaacc ctaaaataaa aattcaaaat
1381 gattggagac tactcggttaa tagacattga aaacgatgaa atctcggtac gtttttatat
1441 tttttgaact gtaatatatt tatgcagaag cggttttgta atgggcccac aaaaaaaaaag
1501 tggtttttga atgyatatga ttccggtcta ttctggaaat ggtctcaaaa agtagagttg
30 1561 agatctcaat acgaaaatga accctttcgt ttgatttatc aaagcctttt attttgaaaa
1621 cgttaaatcc tcactaggat ctctctt

35 MAVFRSTLVLLIIVCLTTY
ELHVHAADGAKVGEVVKID
CGGRCKDRCSKSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGGRKCP**
40

K. At5g15230 (GASA4)

5 1 aaatattcac cctaaaaatga atctaaaaaat gtacaaaaatc acaggaaaaat aaaactaagc
61 agaaatgtcc taagaaaact aaagtttttta aaaaataatc ttcaaagaga tactccaact
121 ggtgtttataa gcaaaaacttg atztatcaaaa aacagggttca tagtatttta tatttagtac
181 tataagcttt ccttaaaacca tgtgcaaaaac catctaccgc agtctaatta ccaatagcaa
241 gtaataaaaat gggactaaca ttggaggcat acgtggaata atataattgg aggaatacag
301 taataatgat atgtgttgcc acagggaata attgatacga gcaaatgtgt gtatatatag
10 361 cttatatgca acatcattgg gtcctcaacc aaaaactcct ctctcagtac actcttttct
421 atacctcaag agactaaaac tagtttgagg agatttagag gagtgtttgg ttctttggat
481 aacaatatcc caactgaaa ATGGCTAAGT CATATGGAGC TATCTTCCTC TTGACCCCTCA
541 TTGTCTCTT CATGCTTCAA ACCATGgtaa cacctctatt atttttttct tctttcaatg
601 tttgaataata ttgaagataa tatatttgat tgttttcctt attgacgaac gatatgagac
15 661 aaatgtgggt tctattattg tacttttagt tggaatataat ttaatttagc ctttttaatg
721 aaattaatttt tacttgtttt tcctctctct ttttttcgtt tttttagGTTA TGGCCTCAAG
781 TGGATCTAAT GTGAAGTGGA GCCAGgtcag ttttattatt gaatcgacta gtaattacct
841 tttaaacat attttatacc tattgttatc tcgtaactta acgaaaagtg attaattagt
901 tacctttttt ggttaatttt cagAAACGTT ATGGACCAGG AAGCCTGAAA CGTACCCgta
20 961 agtttttttct tcacagctat tcttaaacaa ttttttttta atctcataat cgacgaaaaa
1021 taaacaattc aagaaatcct ttattgtgtt ataataaaaa aaaataagca tttcagttgc
1081 agaaaaataag ttgaaagtga agtgttaagt ggactgtttg gtcagatccg tagactcaaa
1141 atataattaga tattgacgaa attgcccctt aatatggtca tacagtcaaa gcaaccact
25 1201 atcttgagac ccacaaaaca gtaaaaaaa aagctaataga atttccacta gattctgttg
1261 ttttttattag taataaaaaa tttttgagtg ttaacatttt gatattgttt gtatttgaaa
1321 caaccagAAT GCCATCGGA ATGTGATAGG AGGTGTAAAA AGACACAGTA CCACAAGGCT
1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGTCTCT GTGTGCCTCC GGGTFACTAT
1441 GGGAACAAAC AAGTTTGCTC CTGCTACAAC AACTGGAAAA CTCAAGAGGG TGGACCAAAA
30 1501 TGCCCTTGAA aaaatctccc ttcgttccct ttttataata aaaattttca actataacta
1561 aatttccttt gatcaatggt ttatctactt tattcctaata gttgtaatgt tatgtcactc
1621 cttttcggat ttgtttctaa atcctaaaaa aaatgagagt ggccctatga atgatatttt
1681 tcatgaatac ttgtgtttct aaagataatt tcccattcat ccacaaaaaa aaaagatatt
1741 ttccatttcg aaaatagtaa tactataaaag ggttaaggcaa accaaataat acaatttaaa
35 1801 aaattcctgc gaaagaagta tgcatatgta gaaaagagtg acattgggtc tctcggccca
1861 gtactaaaaa gccattatt gatttttcca agctttttac aaaatcacgt gttctaacgc
1921 gattgctttt tgccgcaatc ttcttttata caagaattgg gctttgggca gttggaata
1981 aataacgaca acgatatttt acaatcggg

MAKSYGAIFLLTLIVLFMLQTMV

40

MASSGSNVKWSQKRYGPGSLKRTQ

CPSECDRRCKKTQYHKACITFCNKCCRKCLCVPPGYYGKNQVCSCYNNWKTQEGGPKCP**

45

L. At5g14920

```

5      1 ttgctcaactg gtgcaataat cgaagtgaag agcctcttta tatgaaatat ataagcgaca
      61 cagccttatg ggcaaatcga atgctattta tttatttgat aagaagatta ataatttcaa
121    tttgtcatcc actagtctct tggggtaactc aaaacatata accaaaaagt ccatagagtt
181    atttgttctt atttactgat aaagtattcc aagttgatgt acgaataaag tggcaatttc
241    atgtattatc aatataatcc atttttggga atctgatatt ttgtttatcc tcgagctctg
301    agagatatat tttgtgagcag tgaaggttca aagctggcat gcatgatgca tataataact
10     361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat atgggttaata
      421 aataagggaac ttctatttat atcacaaaag gtcactggtc ttcttcgtgt gacttcacca
      481 ctttctcatc tcccacaaaa ATGGCTCTCT CACTTCTTTC AGTCTTTATC TTTTCCATG
      541 TCTTTACCAA Tgtaagttat tcttactttt cataacaaaa ggtgttatta tgttaaagac
      601 tacataatag tatacaatta tgtgcattac gttttcgcgt attgtaacta actatgtatt
15     661 ttgattaatc accgagcagG TTGTTTTTGC TGCTTCAAAT GAGGAATCCA ACGCCTTAGt
      721 acgtttttcta atttccagtt taattatttc tatgcgtctt taactatata ctcaggcatt
      781 tttattgatt attgtgtatg aagttaaatt ttggtatatg tttgtattaa atttatagGT
      841 TTCTTTACCA ACGCCAACAC TTCCATCGCC ATCTCCGGCT ACCAAACCGC CGTCGCCCAG
20     901 TCTCAAACCG CCGACGCCGT CGTACAAGCC ACCCACGCTG CCAACTACTC CTATTAAACC
      961 ACCCACACA AAACCTCCGG TCAAACCTCC AACTATTCCG GTTACACCAG TAAACCTCC
1021   GGTTCAACT CCTCCGATCA AACTACGCC GGTACAACCA CCTACGTACA AACCCCAAC
1081   GCCAACAGTT AAACCCCGT CCGTCCAACC ACCTACGTAC AAACCCCAAA CTCCAACGGT
1141   TAAACCACCC ACTACATCAC CGGTTAAACC ACCCACTACG CCACCAAGTC AATCACCGCC
25     1201 GGTCCAACCA CCTACGTACA AACCCCAAC GTCACCGGTT AAACCACCA CCACAACCTC
      1261 ACCGGTTAAA CCCCCACCA CGACGCCACC GGTCCAACCA CCTACGTACA ATCCCCAAC
      1321 TACACCGGTT AAACCACCTA CAGCGCCGCC TGTCAAACCT CCAACACCAC CTCCCGTAAG
1381   AACTCGGATA Ggtaataata attttctttc aaaagtgtga tgattatcgg tegtgtatta
1441   gatcggatgt ataattggac taaattttgg acggtttagA TTGCGTGCCT TTATGTGGGA
1501   CGAGGTGTGG GCAACACTCG AGGAAGAACG TATGTATGAG AGCGTGCGTC ACGTGCTGCT
30     1561 ACCGCTGCAA GTGTGTTCCC CCAGGCACCT ACGGTAATAA GGAGAAGTGT GGATCTTGTT
      1621 ACGCCAACAT GAAGACACGT GGTGGAATAA CCAAATGTCC TTGAaccttt atatgacgat
      1681 ggttgtttaa cgaataaatt taaatcaatg gagtttttat aagtttgtaa tgcgtttgtt
      1741 tttgttatag taatattgag ttggatcttt gtttacggga cgtagaatac taaataatga
35     1801 aaaaaaacctt ctogatgaat taagggtttt atgaatttgt tttgtattga ataatatagg
      1861 gatggataaa gttttattat tctaacaggt tactttatta ggcatttctt cggctcatgt
      1921 aactcttgta tcgctgaaac tatgtaatat atagaagaac ctaaaaaag aaagaaaaca
1981   agaaatgcac atagcgaagc tcaaaaagat agtgttctgc tagcggtaat gttgttatcc
2041   agttgggtca aatgctctaa ttgcaaatct tatttgggcc ttatatagac tcttatgtgc
2101   atatggtcca gcctatttgg gccgatgtgt ttgaagatca tttgggaaag tcttgcgcaa
40     2161 ggaag

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MALSLLSVFIFHFVFTNVVFAAS

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45     NEESNALVSLPTPLPSPSPA
      TKPPSPALKPPTPSYKPPTLP
      TTPIKPPTTKPPVKPPTIPVT
      PVKPPVSTPPIKLPPVQPPTY
      KPPTPTVKPPSVQPPTYKPPT
50     PTVKPPTTSFVKPPTTPPVQS
      PFVQPPTYKPPTSPVKPPTTT
      PFVKPPTTTPPVQPPTYNPPT
      TPVKPPTAPPVKPPTPPFVRT
      RID
55     CVPLCGTRCGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSKCP*

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M. At5g59845

5 1 gacttgagta tgaatccaat aaccccaaat ttatgcagat tttagaatac ttcttataaa
61 tctttaaata gaataacaac
121 agattctaca tgacatttta aatcactaaa actcttttga aatcataaac caataacaac
181 cccttagttt ttactatatt gaattctgac gtactttttt attagttgaa ttctataaaa
241 tgagaaaaca ttaattatct cttaatcttt gaacttaagc cccacaaaaa tcttataaat
301 tgggacagat ggactagata acaagcgttt cactactcc aaaatttccc tataagtaac
10 361 tctttttgta acctcctttt ctcccaaac catcactcct ttgcatgtgt gtgaaacctt
421 cgagttttct ctcatcttc tcaaagtaac aaactttctc caaacagatt attattaaaa
481 caatctcacc aagaactacg ATGAAATTCC CGGCTGTAAA AGTCTTATT ATCTCTTTC
541 TCATCACATC TTCTTTGTTC ATACTCTCAA CCGCGGATTC GTgtaagtat acacaatgca
601 ttttcttatt ttagatactt ttctcattag aaatttagct ttcttaataa aattgtattg
15 661 tgatgatgga ttaattagCA CCATGCGGAG GAAAATGCAA CGTGAGATGT TCAAAGGCAG
721 GAAGACAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG
781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT
841 CCAAAGGCAC GTCCAAATGT CCTTGATcat gttcttaaga ttatccttat agacacaata
901 tcttgaaatg ttaagattgt gcttgatgcc taaaataatg agcttgagat acttctatga
20 961 atgaatatgt gaaagatttt gacaataaaa tgatttgatg tattaataa ttcttagtga
1021 agttatatat gtataaatga agtatgaaat atacattgta tgttgcttta catgagaaag
1081 ataatctac aacaatccaa tgtatgaaaa ttttactaag ttaactgac agaaacgtta
1141 attatgggtt agaattctgt ggagagatga ttacttttgt aagagaaatt gattgtttgt
1201 tgtcaatgag gataaagtaa gaagccattt ctcaacacat ggacttgata gcaaaactaaa
25 1261 caaggtctaa gcattgaaat tgaaacgtct cgatagataa gattggctca agaaaagcaa
1321 gtgttttttg ttgtagaaaa cagaaattga aattactgtc tacttt

30 **MKFPVAVKVLIIISLLITSSLFILSTA**

DSSP

CGGKCNVRC SKAGRQDRCLKYCNICCEKCN YCVPSGTYGNKDECP CYRDMKNSKGTSKCP*

35

N. At3g10170

genomic structure before splicing and processing 5'- towards 3'
predicted orf sequences are underlined

5
10
15
20

CTGTTTTAGAAAATGGCAACAAAACCTTAGCATCATTGTTTTCTCCATTG
TTGTGTTACATCTTCTTCTGTCTGCCCATATGCATGTAAGTGTTCACA
CTCTATTCTCTATGTTTACATTTTATCAACTTTATCTTATACGTCCCTGA
ATAAAACACAGCCTATATACTTGAATCTCCTGCTCGACAACCACAACCA
CCACAGTCGCAACCACAACCTGCCGCATCACAATAACTCTCAAGTGAGTTT
CTCGGTTTCATCACTACTCAAAAAAGAGTTTCATCGAATCTACAAAACCT
TTTTAACATCCTTTGCATCTTCTTGTGATTTGGCAGTACGGTACTACT
CAAGGCAGTCTTCAACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA
ATTAATGTTTGTGCTGAATGCGAACTAAATCCGCTATCCACCTTTATT
AGAGTGCAGGCAAGGTGTGGAGATAGATGCTCGAATACACAATAACAAGA
AGCCGTGTTTGTCTTCTGCAACAAATGTTGTAACAAGTGCTTGTGTGTG
CCCCAGGTACTTATGGCAATAAGCAAGTATGTCTTGCTATAACAACCTG
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA
CTTTAGCATAACTCCATGTAATTTGTTAATCTACCTATCATAATTTATA
TATGTATTGGACTCTTCCATAATCACATCAGTTCTCTGTGATTATGACGT

Amino acid sequence of the predicted pre-pro-peptide
the first line represents the signal sequence
the second (set of) lines represents the the pro-peptide
the last line represents the conserved Cysteine motif.

MATKLSIIVFSIVVLHLLLSAHMH

FLINVCAECETKSAIPPLLE

CGPRCGDRCSNTQYKKPCLEFFCNKCCNKCLCVPPGTYGNKQVCPCYNNWTKSGGPKCP*

They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cysteine residues.

The consensus of this last domain is:

C-C-RC-----C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP*

(-) = any amino acid;

(C) = conserved C-residue

(/) = either one or the other amino acid at this position;

* = stopcodon

Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis thaliana* (Plant Mol. Biol. 36 (1998). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different members, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).

Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in *arabidopsis* and in rice:

Gene code	contig	gene prediction in At database	<i>Oryza sativa</i> japonica contig	approximate position in bp around:
RKS0	At1g71830 f14o23	ok	OSJNBa0036B21	52.000
RKS1	At1g60800 f8a5	ok	P0038C05	60.000
RKS2	At5g65240 mqn23	ok	OJ1212_C08	8000
RKS3	At5g63710 mbk5	ok	see rks2	
RKS4	At2g23950 t29e15	wrong, exon missing	P0708B04	35.000
RKS5	At5g45780 mra19	wrong, exon missing	OJ1077_A12	102.000
RKS6	At5g10290 wt e 23	ok	see rks2	
RKS7	At5g16000 ku e 24	ok	P0038C05	60.000
RKS8	At1g34210 f23m19	ok	OJ1134_B10	90.000 & 1000 2
different genes!				
RKS10	At4g33430 en d 25	wrong, exon missing	see rks0	
RKS11	At4g30520 wu d 20	wrong, exon missing	see rks4	
RKS12	At2g13800 f13j11	wrong, exon missing	see rks10	
RKS13	At2g13790 f13j11	ok	P0633E08	36.000
RKS14	At3g25560 mw12	wrong, exon missing	OSJNBb0015G09	36.000
ELS1	At5g21090 ch e 52	ok	P0003H10	53.000
ELS2	possibly allelic variant of ELS1 no genomic sequence identified yet			see els1
ELS3	At3g43740 by c 21	ok	P0468B07	52.000

Homology between aa sequences from *arabidopsis* proteins are compared with the rice databases using:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
 protein sequences based on *Oryza sativa japonica* contig sequences.

Arabidopsis thaliana ELS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```

ttactctcaaattccttttcgatttcctctcttaaacctccgaaagctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAACCTAA
CCTTAGCTTTGATTACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTCTA
CGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGTCTC
AAGCAATGATTTGTGTGGACAATCCCACAAAACGGACCCTTTGCTCACATTCC
TTTACAGAACTTTGAGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGT
CTTGCAAGCTACGACACTAACTGCACCTGAacaactggcaaaacctgaaaat
gaagaattggggggtgaccttgtaagaacacttcaccactttatcaaatac
acatctactatgtaataagtatatatatgtagtccaaaaaaaaaaaaaaaaaa

```

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL
TLTLALIHIVEANSEG

10

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA

15

P ELGKLEHLQYLELYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT

Arabidopsis thaliana ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 aaaattactcaaattcctattagattactctcttcgacctccgatagctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAA
CCTTAGCTTTGATTCACCTGGTCTGAAGCAAACCTCCGAAGGAGATGCTCTTTA
CGCTCTTCGCCGGAGTTTAAACAGATCCGGACCATGTCCTCCAGAGCTGGGAT
CCAACCTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
15 ACCGCGTCACTCGTGTGGATTGTTGGGGAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAAC
AACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTTACGGCTTAATGACAACCGATTGACGGGG
20 CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAGTTGTGGATGTC
TAAGCAATGATTTGTGTGGAACAATCCCAACAAACGGACCTTTTGCTCACAT
TCCTTTACAGAACTTTGAGAACAACCCGAGGTTGGAGGGACCGGAATTACTC
GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaaattggcaaaacctga
aaatgaagaattgggggggaccttgtaagaacacttcaccactttatcaaat
25 atcacatctactatgtaataagtatatatatgtagtccaaaaaaaaaatgaa
gaatcgaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt
atgaaaattaaagattgtactgtaatgttcggttggtgggattctgagaagta
acatttgattggtatggtatcaagttgttctgccttgctctgcaaaaaaaaa

30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as
35 described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELEFAASL
ILTLALIHLEVEANSEG

10

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSGHLA

P ELGKLEHLQYLQLYKNNIQGTI
PSELGNLKNLISLDLYNNNLGTIV
PTSLGKLKSLVFLRLNDNRLTGPI
20 PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

25

Arabidopsis thaliana ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctctccggcgaaaacc**ATGGTGGCGCAAAACAGTCGGCGGGAGCTTCTAGCAGCTT**
 CCCTGATCCTAACTTTAGCTCTAATTCGTCTAACGGAAGCAAACCTCCGAAGGGGACGCTC
 TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTTTCAGAGTTGGGATCCAA
 CTCTTGTTAATCCTTGTAAGTTGGTTTCATGTCACTTGTAATCAACACCATCAAGTCACTC
 GTCTGGATTTGGGGAATTCAAACCTTATCTGGACATCTAGTACCTGAACTTGGGAAGCTTG
 15 AACATTTACAATATCTTGAACCTCTACAAAACGAGATTCAAGGAACTATACTTCTGAGC
 TTGGAAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACAACAATCTCACCGGGAAAA
 TCCCATCTTCTTTGGGAAAATTGAAGCGGCTTAACGAAAACCGATTGACCGGTCCTATTC
 CTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTTGT
 GTGGAACAATTCCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAACTTTGAGAACA
 20 ACCTGAGATTGGAGGGACCAGAACTACTAGGTCTTGCGAGCTATGACACCAATTGCACTT
AAaaaagaagttgaagaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a

30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each

35 approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL
ILTLALIRLTEANSEG

5 DALHALRRSLSDP
DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV
10 P ELGKLEHLQYLELYKNEIQGTI
PSELGNLKSLSLDLYNNNLTGKI
P SSLGKLKRLNENRLTGPI
PRELTVISSLKVVDVSGNDLCGTI
PVEGPFEHIPMQNFENNLRLLEGPE
15 LLGLASYDTNCT

Arabidopsis thaliana RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atttttatttttatttttttactctttgtttgttttaatgctaataagggttttttaaagggtt
atcgaaaaaatgagtgagtttgtgttgaggttgtctctgtaaagtgttaatggtggtgat
tttcggaaggttagggttttctcgatctgaagagatcaaatcaagattcgaaatttacca
ttgttgtttgaa**ATGGAGTCGAGTTATGTGGTGT**TTATCTTACTTTCACTGATCTTACTT
CCGAATCATTCACCTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTGCATACTTTG
15 AGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAGCTGGGATCCTACGCTAGTGAAT
CCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAACAGTGTCAAGAGTTGATTG
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAG
TATTTGGAGCTTTACAGTAACAACATAACTGGCCCGATTCCCTAGTAATCTTGGAAATCTG
ACAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCTATTCCGGAATCA
20 TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGGCTTAACAACAACAGTCTCACTGGGTCA
ATTCCTATGTCACTGACCAATATTACTACCCCTCAAGTGTTAGATCTATCAAATAACAGA
CTCTCTGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGTTTGTCT
AATAACTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCCTGGATCTCCCCCGTTT
TCTCTCCACCACCTTTTATTCAACCTCCCCAGTTTCCACCCGAGTGGGTATGGTATA
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCCTGCA
ATAGCCTTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTTTCTTCGATGTCCCTGCC
GAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTTCTTTGCGGGAGCTACAA
GTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTC
TACAAGGGACGCTTGGCAGACGGAACCTTGTGCTGTCAAGAGACTGAAGGAAGAGCGA
30 ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT
CGAAACCTGTTGAGATTACGAGGTTTCTGTATGACACCGACCGAGAGATTGCTTGTGTAT
CCTTACATGGCCAATGGAAGTGTGCTTCGTGTCTCAGAGAGAGGCCACCGTCACAACCT
CCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTAC
CTACATGATCACTGCGATCCGAAGATCATTACCGTGACGTAAAAGCAGCAAACATCCTC
35 TTAGACGAAGAATTGGAAGCGGTTGTTGGAGATTTGCGGTGGCAAAGCTTATGGACTAT
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCATCGGTACATCGCTCCAGAATAT
CTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTTCGGATACGGAATCATGCTTCTA
GAACTAATCACAGGACAAAGAGCTTTGATCTCGCTCGGCTAGCTAACGACGACGACGTC
ATGTTACTTGACTGGGTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT
40 CCAGATCTTCAAACAACTACGAGGAGAGAGAACTGGAACAAGTGATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGTTGAGATTTTGAGGGAA
GAGATTGATTTGAGTCCTAATCCTAACTCTGATTGGATTCTTGATTCTACTTACAATTTG
CACGCCGTTGAGTTATCTGGTCCAAGGTAAaaaaaaaaaaaaaaaaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt *et al.* 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MESSYVVFILLSLILLPNHSL
WLASANLEG

DALHTLRVTLVDP

35

NNVLQSWDPTLVN

PCTWFHVTCNNENSVIRV

DLGNAELSGHLV

40

P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI
PESLGKLSKLRFLRLNNNSLTGSI
PMSLTNITTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

5

TSHPCPGSPPFSPPPP
FIQPPFVSTPSGYGITG

AIAGGVAAGAAL

10

PFAAPAIAFAWW

RRRKPLDIFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

15

DGFSNKNILGRGGFGKVYKGRAD
GTLVAVKRLKEERTPGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPPSQPPLDWPTRKRIALGSA

20

RGLSYLHDHCDPKIIHRDVKAA
NILLDEEFEEAVVGDFGLAKLMD
YKDTHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGIMLLELI
TGQRAFDLARLANDDDVMLLDW

25

VKGLLKEKKLEMLVDPDLQTN
EERELEQVIQVALLCTQGSPME
RPKMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS

30

PNPNSDWILDSTYNLHAVELSGPR

Arabidopsis thaliana RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ccaaagttgattgctttaagaagggat**ATGGAAGGTGTGAGATTTGTGGTGTGGAGATTA**
GGATTTCTGGTTTTTGTATGGTTCTTTGATATCTCTCTGCTACACTTTCTCCTACTGGT
GTAAACTATGAAGTGACAGCTTTGGTTGCTGTGAAGAATGAATTGAATGATCCGTACAAA
GTTCTTGAGAATTGGGATGTGAATTCAGTTGATCCTTGTAAGTGGAGAATGGTTTCTTGC
ACTGATGGCTATGTCTCTTCACTGGATCTTCCTAGCCAAAGCTTGTCTGGTACATTGTCT
15 CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTGCAAAACAATGCAATCACT
GGTCCAATTCCGAAACGATTGGGAGGTTGGAGAAGCTTCAGTCACTTGATCTTTCGAAC
AATTCATTACCGGGGAGATACCGGCCTCACTTGGAGAACTCAAGAACTTGAATTACTTG
CGGTAAACAATAACAGTCTTATAGGAACCTGCCCTGAGTCTCTATCCAAGATTGAGGGA
CTCACTCTAGTCGACATTTTCGTATAACAATCTTAGTGGTTCGCTGCCAAAAGTTTCTGCC
20 AGAACTTTCAAGGTAATTGGTAATGCGTTAATCTGTGGCCCAAAGCTGTTTCAAACGTG
TCTGCTGTTCCCGAGCCTCTCACGCTTCCACAAGATGGTCCAGATGAATCAGGAACCTCGT
ACCAATGGCCATCACGTTGCTCTTGCATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGT
TTCTTTACAAGCGGAATGTTTCTTTGGTGGAGATATCGCCGTAACAAGCAAATATTTTTT
GACGTTAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATTC
25 AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGA
TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACTTTGGTGGCTGTCAAACGTCTC
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGA
ATTTTAGTCTACCCTTACATGCCAAATGGGAGTGTGCGATCACGCTTAAAGATAATATC
30 CGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA
GGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA
GCTAACATTCTGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTAGCTAAG
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAGTGTGGCCACATT
GCACCTGAGTACTTATCCACGGGTCAGTCTCAGAGAAGACTGATGTCTTTGGCTTTGGC
35 ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTCTTGATTTTGGCAGATCCGCACAC
CAGAAAGGTGTAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAAACTAAAGCAG
TTAATAGACAAAGATCTAAATGACAAGTTTCGATAGAGTAGAACTCGAAGAAATCGTTCAA
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACCGAAAATGTCAGAAGTTATG
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT
40 GAGCATCAGCCACCGCCATTGCCACCGGGGATGGTGAGTTCTTCGCCGCGTGTGAGGTAT

TACTCGGATTATATTCAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT
CGATGAttatgactcactgttttttaaaaaa

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVRFVWRLGFL
VFVWFFDISSATLSPTGVNYEV

TALVAVKNELNDP

35

YKVLENWDVNSVD

PCSWRMVSCDGYVSSL

DLPSQSLSGT
LSPRIGNLTYLQSVLQNNAITGPI
PETIGRLEKLQSLDLSNNSFTGEI
PASLGELKNLNYLRLNNNSLIGTC
5 PESLSKIEGLTLVDISYNNLSGSL
PKVSARTFK VIGNALICGPK

AVSNCSAVPEPLTL
PQDGPDESGTRTNG
10
HHVALAFAASF
AAFFVFFETSGMFLWW

RYRRNKQIFFDVNEQYDPE
15 VSLGHLKRYTFKELRSAT

NHFNSKNILGRGGYGIVYKGHLND
GTLVAVKRLKDCNIAGGEVQFQ
TEVETISLALHRNLLRLRGFCS
20 SNQERILVYPMPNGSVASRLK
DNIRGEPALDWSRRKKIAVGTA
RGLVYLHEQCDPKIIHRDVKAA
NILLDEDFEAVVGDFGLAKLLD
HRDSHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGQKALDFGRSAHQKGVMLDW
VKKLHQEGKLKQLIDKDLNDKF
DRVELEEIVQVALLCTQFNPSH
RPKMSEVMKMLE
30
GDGLAERWEATQNGTGEHQPPPLPPGMVSS

PRVRYYSYIQESSLVVEAIELSGPR
35

Arabidopsis thaliana RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

10

tcaatttttggtagctcttagaaaa**ATGGCT**CTGCTTATTATCACTGCCTTAGTTTTTAGT
AGTTTATGGTCATCTGTGTCACCAGATGCTCAAGGGGATGCATTATTTGCGTTGAGGAGC
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAGAATCAAGTCGATCCTTGT
ACTTGGTCTCAAGTTATTTGTGATGACAAGAAACATGTTACTTCTGTAACCTTGTCTTAC

15

ATGAACTTCTCCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAACCTCTCAAGACT
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAATCCATTGGAAATCTGTCT
AGCTTGACCAGCTTAGATTTGGAGGATAATCACTTAACTGATCGCATTCCATCCACTCTC
GGTAATCTCAAGAATCTACAGTTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT
ATCCCGGATTCACTTACAGGTCTATCAAACTGATAAATATTCTGCTCGACTCAAATAAT

20

CTCAGTGGTGAGATTCCTCAGAGTTTATTCAAAATCCCAAATACAATTTACAGCAAAC
AACTTGAGCTGTGGTGGCACTTTCCCGCAACCTTGTGTAACCGAGTCCAGTCTTCAGGT
GATTCAAGCAGTAGAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT
CTACTAGGATTCTTCTTCTTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC
GTATTTGTGGATGTTGCAGGAACGAACCTTTAAAAAAGTTTGATTTCAAGGTGAAGTGGAC

25

AGAAGGATTGCTTTTGGACAGTTGAGAAGATTTGCATGGAGAGAGCTTCAGTTGGCTACA
GATGAGTTCAAGTAAAAGAATGTTCTCGGACAAGGAGGCTTTGGGAAAGTTTACAAAGGA
TTGCTTTTCGGATGGCACCAAAGTCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGA
GGAGATGAAGCTTTCCAGAGAGAAGTTGAGATGATAAGTGTAGCTGTTCATAGGAATCTG
CTTCGCCTTATCGGCTTTTGTACAACACAACTGAACGACTTTTGGTGTATCCTTTCATG

30

CAGAACTAAGTGTTGCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT
TGGTTCAGGAGGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAATATCTTCATGAA
CATTGCAACCCGAAGATCATAACAGAGATGTGAAAGCTGCAAATGTGTTACTAGATGAA
GACTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAGTTGGTAGATGTTAGAAGGACT
AATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGCACCAGAATGTATATCCACA

35

GGGAAATCGTCAGAGAAAACCGATGTTTTCGGGTACGGAATTATGCTTCTGGAGCTTGTA
ACTGGACAAAGAGCAATTGATTTCTCGCGTTAGAGGAAGAAGATGATGTCTTATTGCTA
GACCATGTGAAGAACTGGAAAAGAGAGAAGAGATTAGAAGACATAGTAGATAAGAAGCTT
GATGAGGATTATATAAAGGAAGAAGTTGAAATGATGATACAAGTAGCTCTGCTATGCACA
CAAGCAGCACCGGAAGAACGACCAGCGATGTCGGAAGTAGTAAGAATGCTAGAAGGAGAA

40

GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAATCTTGAAGTGACGAGACAAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCCATTAATAATCAAGATGCTATT
GAATTATCTGGTGGAAGATAGaaacaaaaaa

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
30 product.

MALLIITALVFSSL
WSSVSPDAQG

35 DALFALRSSLR
ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTSV

TLSYMNFSS GTLSSGI
G ILTTLKTLTLKGNIGIMGGI
PESIGNLSSLTSLDLEDNHLTDRI
5 PSTLGNLKNLQFLTLSRNNLNGSI
PDSLTGLSKLINILLDSNNLSGEI
PQSLFKIPKYN FTANNLSCGG

TFPQPCVTESSPSGDSSSRKTG
10 IIAGVVSGIAVIL
LGFFFFFFFC

KDKHKGYKRDFVFDVAGTNFKKGLISGE
15 VDRRIAFGQLRRFAWRELQLAT

DEFSEKNVLGQGGFGKVYKGLLSD
GTKVAVKRLTDFERPGGDEAFQ
REVEMISVAVHRNLLRLIGFCT
20 TQTERLLVYPFMQNLSVAYCLR
EIKPGDPVLDWFRRKQIALGAA
RGLEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD
VVRTNVTTQVRGTMGHIAPECI
25 STGKSSEKTDVFGYGIMLLELV
TGQRAIDFSRLEEEDDVLLLDH
VKKLEREKRLIEDIVDKKLEDEY
IKEEVEMMIQVALLCTQAAPEE
RPAMSEVVRMLE
30 GEGLAERWEEWQNLEVTRQEEFQ

RLQRRFDWGEDSINNQDAIELSGGR
35

Arabidopsis thaliana RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
aacggtgaaagtttccatgatcctcttcgaggattcattcaaagaaattgctttagatgg
10 aacaatcagaaattgatcttacaatgtttcATGGCCTTAGCTTTTGTGGGAATCACTTCG
TCAACAACTCAACCAGATATCGAAGGAGGAGCTCTGTTGCAGCTCAGAGATTCGCTTAAT
GATTCGAGCAATCGTCTAAAATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT
TATGTTACCTGCAGAGGCCAGAGTGTGTGGCTCTAAATCTTGCCTCGAGTGGATTACACA
GGAACACTCTCTCCAGCTATTACAAAACTGAAGTTCTTGGTTACCTTAGAGTTACAGAAC
15 AATAGTTTATCTGGTGCCTTACCAGATTCTCTTGGGAACATGGTTAATCTACAGACTTTA
AACCTATCAGTGAATAGTTTCAGCGGATCGATACCAGCGAGCTGGAGTCAGCTCTCGAAT
CTAAAGCACTTGGATCTCTCATCCAATAATTTAACAGGAAGCATCCCAACACAATTCTTC
TCAATCCCAACATTCGATTTTTCAGGAACTCAGCTTATATGCGGTAAAAGTTTGAATCAG
CCTTGTTCTTCAAGTTCTCGTCTTCCAGTCACATCCTCCAAGAAAAGCTGAGAGACATT
20 ACTTTGACTGCAAGTTGTGTTGCTTCTATAATCTTATTCCTTGGAGCAATGGTTATGTAT
CATCACCATCGCGTCCGCAGAACCAAATACGACATCTTTTTTGATGTAGCTGGGGAAGAT
GACAGGAAGATTTCTTTGGACAACTAAAACGATTCTCTTTACGTGAAATCCAGCTCGCA
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTTGGTAAAGTATACAGA
GGTTTGCTTCCAGACAAAACAAAAGTTGCAGTGAACGCCTTGCGGATTACTTCAGTCCT
25 GGAGGAGAAGCTGCTTTCCAAAGAGAGATTCAGCTCATAAGCGTTGCGGTCATAAAAAT
CTCTTACGCCTTATTGGCTTCTGCACAACTTCTCTGAGAGAATCCTTGTTTATCCATAC
ATGGAAAATCTTAGTGTTGCATATCGACTAAGAGATTTGAAAGCGGGAGAGGAAGGATTA
GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC
GAACATTGTAACCCGAAGATCATAACCGCGATCTCAAGGCTGCAAACATACTTTTAGAC
30 AACAATTTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG
ACTCATGTCACAACTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTATCTCTGC
ACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCTTGAGCTT
GTTACTGGTCAGCGCGCAATCGATTTTTCAGCTTGGGAAGAGGAAAATATTCTCTTG
CTTGATCATATAAAGAAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT
35 TTGACTACATATGACTCCAAAGAAGTTGAAACAATCGTTCAAGTGGCTCTTCTCTGCACA
CAAGGCTCACCAGAAGATAGACCAGCGATGTCTGAAGTGGTCAAATGCTTCAAGGGACT
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACAACTTGAAGAAGTTAGGAACAAAGAA
GCATTGTTGCTTCCGACTTTACCGGCTACTTGGGATGAAGAAGAAACCACCGTTGATCAA
GAATCTATCCGATTATCGACAGCAAGATGAagaagaaacagagagagaaagatatctatg
40 aaaa
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each
15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular
20 domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth
25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSTTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLS

P AITKLKFLVTLELQNNLSGAL

PDSLGNMVLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI
PTQFFSIPTFEFSGTQLICGKS

5 LNQPCSSSRLPVTSSKKKLRD

ITLTASCVASIIL
FLGAMVMYHHH

10

RVRRTKYDIFFDVAGEDDR
KISFGQLKRFSLEIQLAT

DSFNESNLIGQGGFGKVYRGLLPD

15

KTKVAVKRLADYFSPGGEAAFQ
REIQLISVAVHKNLLRLIGFCT
TSSERILVYPYMENLSVAYRLR
DLKAGEEGLDWPTRKRVAFGSA
HGLEYLHEHCNPKIIHRDLKAA

20

NILLDNNFEPVLGDFGLAKLVD
TSLTHVTTQVRGTMGHIAPEYL
CTGKSSEKTDVFGYGITLLELV
TGQRAIDFSRLEEEENILLDD
HIKKLLREQRLRDIVDSNLTTY

25

DSKEVETIVQVALLCTQGSPED
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVNKEALLL

30

PTLPATWDEEETTVDQESIRLSTAR

Arabidopsis thaliana RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tcttccttctccttctggtaatctaataagccttttc**ATGGTGGT**GATGAAGATATTC
TCTGTTCTGTTACTACTATGTTTCTTCGTTACTTGTCTCTCTCTCTGAACCCAGAAAC
CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC
AAAAACTGGGATGAGTTTTCTGTTGATCCTTGTAGCTGGACTATGATCTCTTGTCTTCA
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTTCAGGAACCTTATCTGGG
15 TCTATTGGAAATCTCACTAATCTTCGACAAGTGTCATTACAGAACAATAACATCTCCGGT
AAAATCCCACCGGAGATTTGTTCTCTTCCCAAATTACAGACTCTGGATTTATCCAATAAC
CGGTTCTCCGGTGAAATCCCCGGTTCGTGTTAACCAGCTGAGTAATCTCCAATATCTGTTG
AACAACAACCTCATTATCTGGGCCCTTTCCTGCTTCTGTCTCAAATCCCTCACCTCTCT
TTCTTAGACTTGTCTTATAACAATCTCAGAGGTCCTGTTCTAAATTTCTGCAAGGACA
20 TTCAATGTTGCTGGGAACCTTTGATTTGTAAAAACAGCCTACCGGAGATTTGTTTCAGGA
TCAATCAGTGCAAGCCCTCTTCTGTCTCTTTACGTTCTTCATCAGGACGTAGAACCAAC
ATATTAGCAGTTGCACTTGGTGTAAGCCTTGGCTTTGCTGTTAGTGTAATCCTCTCTCTC
GGGTTCAATTTGGTATCGAAAGAAAACAAGACGGTTAACGATGCTTCGCATTAACAAGCAA
GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAAGCTTCACATTCAGGGAACCTTCATGTA
25 GCTACGGATGGTTTTAGTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTAC
AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAAACGATTGAAAGATGTGAATGGA
ACCTCCGGGAACCTCACAGTTTCGTACTGAGCTTGAGATGATCAGCTTAGCTGTTTCATAGG
AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCCT
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAC
30 ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGAGCAATGC
GATCCAAGATTATTACCGAGATGTCAAGGCAGCAAACATTCTCCTAGATGAGTATTTT
GAAGCAGTTGTTGGGGATTTTGGACTAGCAAAGCTACTCAACCACGAGGATTCACATGTC
ACAACCGCGGTTAGAGGAACTGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCAG
TCATCTGAGAAAACCGATGTCTTTGGGTTTCGGTATACTTTTGCTAGAGCTCATCACAGGA
35 ATGAGAGCTCTCGAGTTTGGCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAATGGGTG
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGGACAACC
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACTCAGTTTCTT
CCAGCTCACAGACCCAAAATGTCTGAAGTAGTTTCAGATGCTTGAAGGAGATGGATTAGCT
GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTACAGG
40 ACTATTACCTCTACTGATGGCAACAACCAAACCAACATCTGTTTGGCTCCTCAGGATTT

GAAGATGAAGATGATAATCAAGCGTTAGATTCATTCGCCATGGAACTATCTGGTCCAAGG
TAGtaaatcttggacacagaaagaaacagatataatatcccatgacttcaatttttgtt

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MVVMKLITMKIFSVLLLLL
CFFVTCSLSSEPRNPEV

EALINIKNELHDP

35

HGVFKNWDEFSVD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI
PPEICSLPKLQTLDLNNRFSGEI
PGSVNQLSNLQYLRLNNNSLSGPF
5 PASLSQIPHLSFLDLSYNNLRGPV
PKFPARTENVAGNPLICKNS

LPEICSGSISASPL
SVSLRSSSGRRTN

10

ILAVALGVSLGFAVSVIL
SLGFIWY

RKKQRRLTMLRINKQEE

15

GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFGNVYRGKFGD

GTVVAVKRLKDVNGTSGNSQFR

TELEMISLAVHRNLLRLIGYCA

20

SSSERLLVYPYMSNGSVASRLK

AKPALDWNTRKKIAIGAA

RGLFYLHEQCDPKIIHRDVKAA

NILLDEYFEAVVGDFGLAKLLN

HEDSHVTTAVRGTVGHIAPEYL

25

STGQSSEKTDVFGFGILLLELI

TGMRALEFGKSVSQKGAMLEW

VRKLHKEMKVEELVDRELGTTY

DRIEVGEMLQVALLCTQFLPAH

RPKMSEVVQMLE

30

GDGLAERWAASHDHSFYHANM

SYRTITSTDGNNQTKHLFG

SSGFEDEDDNQALDSFAMELSGPR

35

Arabidopsis thaliana RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctagagaattcattatactttttctacg**ATGG**GAGATTTCCTTGATGAAGTTTCTGTTTTTA
GGAATCTGGGTTTATTATTACTCTGTTCTTGACTCTGTTTCTGCCATGGATAGTCTTTTA
TCTCCCAAGGTGGCTGCGTTAATGTCAGTGAAGAACAAGATGAAAGATGAGAAAGAGGTT
TTGTCTGGTTGGGATATTAACCTCTGTTGATCCTTGACTTGGAACATGGTTGGTTGTTCT
TCTGAAGGTTTTGTGGTTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT
15 ACTAGTATTGGGAATTAACCTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT
GGTCCGATTCCCTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTTATCGGGG
AATCGGTTTAGTGGTGAAATCCCAGCTTCTTTAGGGTTCTTAACTCACTTAACTACTTG
CGGCTTAGCAGGAATCTTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT
CTTTCTTTCTTGATCTATCTTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA
20 AAAGATTACAGGAAATGCATTTCTTTGTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT
AGCAAACATCACAGCTTAGTGCTCTCTTTTGCAATTTGGCATTGTTGTTGCCTTTATCATC
TCCCTAATGTTTCTCTTCTTCTGGGTGCTTTGGCATCGATCACGTCTCTCAAGATCACAC
GTGCAGCAAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTTCAGTTTTTCGCGAAATA
25 CAAACCGCAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATG
GTTTATAAAGGTATCTCCCAAATGGAAGTGTGGTGGCAGTTAAAAGATTGAAAGATCCG
ATTTATACAGGAGAAGTTCAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTCAC
CGTAACCTTTTACGCCTCTTTGGATTCTGTATGACCCCGAAGAGAGAATGCTTGTGTAT
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC
30 ATTGCACTCGGCGCAGCTCGAGGACTTGTTTACTTGACGAGCAATGCAATCCAAAGATT
ATTCACAGAGACGTCAAAGCTGCAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT
GGCGATTTTGGTCTAGCAAAGCTTTTAGACCAGAGAGATTACATGTCACTACCGCAGTC
CGAGGAACCATTTGGACACATCGCTCCCGAGTACCTTTCCACTGGACAGTCTCAGAGAAA
ACCGATGTTTTCGGATTTCGGAGTACTAATCCTTGAAGTCAATAACAGGTCATAAGATGATT
35 GATCAAGGCAATGGTCAAGTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA
GCAGAGAAGAGATTTGCAGAGATGGTGGACAGAGATTTGAAGGGAGAGTTTGATGATTTG
GTGTTGGAGGAAGTAGTGGAATTGGCTTTGCTTTGTACACAGCCACATCCGAATCTAAGA
CCGAGGATGTCTCAAGTGTGTAAGGTACTAGAAGGTTTAGTGGAACAGTGTGAAGGAGGG
TATGAAGCTAGAGCTCCAAGTGTCTCTAGGAACTACAGTAATGGTCATGAAGAGCAGTCC
40 TTTATTATTGAAGCCATTGAGCTCTCTGGACCACGATGAtagacttcatagtgtcttaac

tagtcttcttgattttgttgtcattgtcatggc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no
10 leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine /
20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
25 protein interactions.

MEISLMKFLFLGIWVYYYS

VLDSVSAMDSLLSPKV

30

AALMSVKNMKDE

KEVLSGWDINSVD

PCTWNMVGCSSEGFVVS

35

LEMASKGLSGILS

T SIGELTHLHTLLQLNNQLTGPI

PSELGQLSELETLDLSGNRFSGEI

PASLGFLTHLNYLRSLRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT
PNISAK DYRKCISLWSSFPR

ALLRCYTCEKCCNR
5 SAATGLSEKDNSK

HHSLVLSFAFGIVV
AFIISLMFLEFFWVLWH

10 RSRLSRSHVQQDYEF
EIGHLKRFSEFREIQTAT

SNFSPKNILGQGGFGMVYKGYLPN
GTVVAVKRLKDPIYTGEVQFQ
15 TEVEMIGLAVHRNLLRLFGFCM
TPEERMLVYPYMPNGSVADRLR
DWNRRISIALGAA
RGLVYLHEQCNPKIHRDVKAA
NILLDESFEAIVGDFGLAKLLD
20 QRD SHVTTAVRGTIGHIAPEYL
STGQSSEKTDVFGFGVLILELI
TGHKMIDQGNGQVRKGMILSW
VRTLKA EKRF AEMVDRDLKGEF
DDLVL EEVVELALLCTQPHPNL
25 RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFII EAIELSGPR
30

Arabidopsis thaliana RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
attgttttccttcttttgggattttctccttggatggaaccagctcaattaatgagatgag
10 ATGAGAATGTTTCAGCTTGCAGAAGATGGCTATGGCTTTTACTCTCTTGTTTTTGCCTGT
TTATGCTCATTTGTGTCTCCAGATGCTCAAGGGGATGCACTGTTTGCCTTGAGGATCTCC
TTACGTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTATTTGTGATGACAAAACTTTGTCACTTCTCTTACATTGTCAGATATG
AACTTCTCGGGAACCTTGTCTTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
15 TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTTGGAGGACAATCAGCTAACTGGTCGTATACCATCCACTATCGGTAAT
CTCAAGAAACTTCAGTTCTTGACCTTGAGTAGGAACAACTTAATGGGACTATTCCGGAG
TCACTCACTGGTCTTCCAAACCTGTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCTTCAAAGTCTGTTTGAGATCCCAAAATATAATTTACGTCAAACAACCTGAAT
20 TGTGGCGGTGCTCAACCTCACCTTGTGTATCCGCGGTTGCCCATTCAGGTGATTCAAGC
AAGCCTAAAACTGGCATTATTGCTGGAGTTGTTGCTGGAGTTACAGTTGTTCTCTTTGGA
ATCTTGTTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTGTG
GATGTTGCAGGTGAAGTGACAGGAGAATTGCATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAATGTACTTGGTCAAGGAGGC
25 TTTGGGAAAGTTTACAAAGGAGTGCTTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTTGAAAGTCCTGGTGGAGATGCTGCTTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGACATCGTCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAAACGGATTGCCTTAGGAGCAGCGCT
30 GGTTTTGAGTATCTTCATGAACATTGCAATCCGAAGATCATAATCGTGATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAAG
CTAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTCGAGGAACAATGGGTACATT
GCACCAGAATATTTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTTACAGGACAACGCGCAATAGACTTTTCACGTTTGGAGGAA
35 GAAGATGATGTCTTGTTACTTGACCACGTGAAGAACTGGAAAGAGAGAAGAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAAGAAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTACACAGAAGACCGACAGTGATGTCTGAAGTT
GTGAGGATGTTAGAAGGAGAAGGGCTTGCGGAGAGATGGGAAGAGTGGCAAAACGTGGAA
GTCACGAGACGTCATGAGTTGAACGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGGAGATGAaccaaaaacatcaaacctt
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown
20 function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAF^TLLFFAC^LCSFVSPDAQG

30

DALFALRISLRALP

NQLSDWNQNQVN

PCTWSQVICDDKNFVTSL

35

TLSDMNFSGTLSSRV

GILENLK^TLT^LLK^GNGITGEI

PEDFGNLTSLTSLDLEDNQLTGRI

PSTIGNLKKLQFLTLNRNKLNGTI
PESLTGLPNLLNLLLDNSNSLSGQI
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTTVL
FGILLFLFC

10 KDRHKGYYRDRVFDVAGE
VDRRIAFGQLKRFAWRELQLAT

DNFSEKNVLGQGGFGKVYKGVLPD
TPKVAVKRLTDFESPGDAAEQ

15 REVEMISVAVHRNLLRLIGFCT
TQTERLLVYPFMQNLSLAHRLR
EIKAGDPVLDWETRKRIALGAA
RGFEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD

20 VRRTNVTTQVRGTMGHIAPEYL
STGKSSERTDVFGYGIMLLELV
TGQRAIDFSRLEEEDDVLLLDH
VKKLEREKRLGAIVDKNLDGEY
IKEEVEMMIQVALLCTQGSPE

25 RPVMSEVVRMLE

GEGLAERWEEWQNVETRRHEFE

RLQRRFDWGEDSMHNQDAIELSGGR

30

Arabidopsis thaliana RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 acatccttggttttctgctcattcctctggttcaaca**ATGG**GAGAGTACTATTGTTATGATGA
TGATGATAACAAGATCTTTCTTTTGCTTCTTGGGATTTTTATGCCTTCTCTGCTCTTCTG
TTCACGGATTGCTTTCTCCTAAAGGTGTTAACTTTGAAGTGCAAGCTTTGATGGACATAA
AAGCTTCATTACATGATCCTCATGGTGTCTTGTATAACTGGGATAGAGATGCTGTTGATC
CTTGTAGTTGGACAATGGTCACTTGTTCCTCTGAAAACCTTTGTCATTGGCTTAGGCACAC
15 CAAGTCAGAATTTATCTGGTACACTATCTCCAAGCATTACCAACTTAACAAATCTTCGGA
TTGTGCTGTTGCAGAACAAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA
CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTTCCACGGTGAAATTCCTTTTTTCAG
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTCTGGAGTGT
TTCTCTGTCACTATCTAATATGACTCAACTTGCCCTTTCTTGATTTATCATAACAACATC
20 TTAGTGGTCCTGTTCCAAGATTTGCTGCAAAGACGTTTAGCATCGTTGGGAACCCGCTGA
TATGTCCAACGGGTACCGAACCAGACTGCAATGGAACAACATTGATACCTATGTCTATGA
ACTTGAATCAAACCTGGAGTTCCTTTATACGCCGGTGGATCGAGGAATCACAAAATGGCAA
TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATTGCTGTTGGTTTTGTTTC
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTTGATGTTAAAGATGGGAATCATC
25 ATGAGGAAGTTTCACTTGGAACCTGAGGAGATTTGGTTTCAGGGAGCTTCAGATTGCGA
CCAATAACTTCAGCAGTAAGAACTTATTGGGGAAAGGTGGCTATGGAAATGTATACAAAG
GAATACTTGGAGATAGTACAGTGGTTGCAGTGAAAAGGCTTAAAGATGGAGGAGCATTGG
GAGGAGAGATTCACTTTCAGACAGAAGTTGAAATGATCAGTTTAGCTGTTTCATCGAAATC
TCTTAAGACTCTACGGTTTCTGCATCACACAACTGAGAAGCTTCTAGTTTATCCTTATA
30 TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGAAGTGGAGCATAA
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC
CGAAGATTATCCACCGCGATGTCAAAGCAGCGAATATACTTCTTGATGACTACTGTGAAG
CTGTGGTTGGCGATTTTGGTTTAGCTAAACTCTTGGATCATCAAGATTCTCATGTGACAA
CCGCGGTTAGAGGCACGGTGGGTACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT
35 CTGAGAAAACAGATGTTTTTGGCTTCGGGATTCTTCTTCTTGAGCTTGTAACCGGACAAA
GAGCTTTTGAGTTTGGTAAAGCGGCTAACCAAGAAAGGTGTGATGCTTGATTGGGTAAAA
AGATTCATCAAGAGAAGAACTTGAGCTACTTGTGGATAAAGAGTTGTTGAAGAAGAAGA
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTTGTGCACACAGTACC
TGCCAGGACATAGACCAAAAATGTCTGAAGTTGTTTGAATGCTGGAAGGAGATGGACTTG
40 CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG
TGCAAGCAATGGAGCTCTCTGGTCCTAGATGAaatctatacatgaatctgaagaagaaga
agaacatgcatctgtttcttgaatcaagagggattcttgtttttttgtataatagagagg
ttttttggaggggaaatgttgtgtctctgtaactgtataggcttgttgtgtaagaagttat
5 tactgcacttaggggtaattcaaagttctttacataaaaaaatgattagttgcgttgaata
gaggggaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaaaaa

10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
20 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
25 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
30 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF
CFLGFLCLLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP
HGVLDNWDRDAVD

PCSWTMVTCSSSENFVIG

5

LGTPSQNLSGTL
SPSITNLTNLRIVLLQNNNIKGKI
PAEIGRLTRLETLDLSDNFFHGEI
PFSVGYLQSLQYLRNNNSLSGVF
10 PLSLSNMTQLAFLDLSYNNLSGPV
PRFAA KTFSIVGNPLICPT

GTEPDCNGTTLIPMSMNL
NQTGVPLYAGGSRNHKMA

15

IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKGNHHE
EVSLGNLRRFGFRELQIAT

20

NNFSSKNLLGKGGYGNVYKGILGD
STVVAVKRLKDGGALGGEIQFQ
TEVEMISLAVHRNLLRLYGFCI
TQTEKLLVYPYMSNGSVA

25

SRMKAKPVLWDSIRKRIAIGAA
RGLVYLHEQCDPKIIHRDVKAA
NILLDDYCEAVVGDFGLAKLLD
HQDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELV

30

TGQRAFEFGKAANQKGVMLDW
VKKIHQEKKLELLVDKELLKKKSY
DEIELDEMVRVALLCTQYLPGH
RPKMSEVVRMLE

35

GDGLAEKWEASQRSDS
VSKCSNRINELMSSS

DRYSDLTDDSSLVQAMELSGPR

40

Arabidopsis thaliana RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 gttttttttttttttaccctcttggaggatctgggaggagaaatttgcttttttttggtaa
ATGGGGAGAAAAAGTTTGAAGCTTTTGGTTTTGTCTGCTTAATCTCACTGCTTCTTCTG
TTTAATTTCGTTATGGCTTGCCTCTTCTAACATGGAAGGTGATGCACTGCACAGTTTGAGA
GCTAATCTAGTTGATCCAAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTTAATCCG
TGTACTTGGTTTTACGTAACGTGTAACAACGAGAACAGTGTTATAAGAGTCGATCTTGGG
15 AATGCAGACTTGTCTGGTCAGTTGGTTCCTCAGCTAGGTCAGCTCAAGAACTTGCAGTAC
TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTTCCAAGCGATCTTGGGAATCTGACA
AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA
GGAAAGCTATTCAAGCTTCGCTTTCTTCGGCTCAACAATAACAGTCTCACCGGACCAATT
CCCATGTCATTGACTAATATCATGACCCTTCAAGTTTTGGATCTGTGCAACAACCGATTA
20 TCCGGATCTGTTCTTGATAATGGTTCCTTCTCGCTCTTCACTCCCATCAGTTTTGCTAAC
AACTTGGATCTATGCGGCCAGTTACTAGCCGTCCTTGTCTGGATCTCCCCCGTTTTTCT
CCTCCACCACCTTTTATACCACCTCCCATAGTTCCTACACCAGGTGGGTATAGTGCTACT
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGCTGCTTTACTATTTGCTGCCCTGCTTTA
GCTTTTGCTTGGTGGCGTAGAAGAAAACCTCAAGAATTCTTCTTTGATGTTCTTGCCGAA
25 GAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAACCTCAAGTA
GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTCGGAAAAGTCTAC
AAAGGCCGTCTTGCTGATGGAACACTTGTTGCAGTCAAACGGCTTAAAGAAGAGCGAACC
CCAGGTGGCGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTACAGA
AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGTTTTATCCT
30 TACATGGCTAATGGAAGTGTGCTTCCTGTTTGAGAGAACGTCCACCATCACAGTTGCCT
CTAGCCTGGTCAATAAGACAGCAAATCGCGCTAGGATCAGCGAGGGGTTTGTCTTATCTT
CATGATCATTGCGACCCCCAAAATTATTCACCGTGATGTGAAAGCTGCTAATATTCTGTTG
GACGAGGAATTTGAGGCGGTGGTAGGTGATTTCGGGTTAGCTAGACTTATGGACTATAAA
GATACTCATGTCACAACGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC
35 TCAACTGGAAAATCTTCAGAGAAAACCTGATGTTTTTGGCTACGGGATCATGCTTTTGGAA
CTGATTACAGGTCAGAGAGCTTTTGATCTTGCAAGACTGGCGAATGACGATGACGTTATG
CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT
GACCTGCAAAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC
TGCACACAGAGCTCACCTATGGAACGACCTAAGATGTCTGAGGTTGTTTGAATGCTTGAA
40 GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTTCTACCCACCTCTGACTGGATCCTTGATTGACTGATAATCTTCAT
GCTATGGAGTTGTCTGGTCCAAGATAAacgacattgtaatttgcctaacagaaaagagaa
agaacagagaaatattaagagaatcacttctctgtattctt

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt *et al.* 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGFVCLISLLLLFNSL
WLASSNMEG

DALHSLRANLVDP
NNVLQSWDPTLVN

35

PCTWFHVTCNNNSVIRV

DLGNADLSGQLV

P QLGQLKNLQYLELYSNNITGPV

40

PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGLKLFKLRFLRLNNSLTGPI
PMSLTNIMTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

5 TSRPCPGSPPFSPPPP
 FIPPPIVPTPGGYSATG

AIAGGVAAGAAL
LFAAPALAFAWW

10 RRRKPOEFFFDVPAEEDPE
 VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRLAD
15 GTLVAVKRLKEERTPGGELQFQ
 TEVEMISMAVHRNLLRLRGFCM
 TPTERLLVYPYMANGSVASCLR
 ERPPSQLPLAWSIRQQIALGSA
 RGLSYLHDHCDPKIIHRDVKAA

20 NILLDEEFEAVVGDFGLARLMD
 YKDTHTTAVRGTIGHIAPEYL
 STGKSSEKTDVFGYGIMLLELI
 TGQRAFDLARLANDDDVMLLDW
 VKGLLKEKKLEMLVDPDLQSNY

25 TEAEVEQLIQVALLCTQSSPME
 RPKMSEVVRMLE

GDGLAEKWDEWQKVEVLRQEVELS

30 SHPTSDWILDSTDNLHAMELSGPR

Arabidopsis thaliana rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggggttttaacaatgatggatctctctgatgagggatagttctaggggtttgtttt
taatctcttgaggataaaa**ATG**GAAACGAAGATTAATGATCCCTTGCTTCTTTTGGTTGATT
CTCGTTTTGGATTTGGTTCTCAGAGTCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT
ACTCCATGTACATGGTTTCATGTTACTTGCAATAGCGACAATAGTGTACACGTGTTGAC
15 CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAAACTTG
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGAAAT
CTGACGGAATTGGTGAGCTTGATCTTTACTTGAACAATTTAAGCGGGCCTATTCCATCA
ACTCTCGGCCGACTTAAGAACTCCGTTTCTTGCGTCTTAATAACAATAGCTTATCTGGA
GAAATTCCAAGGTCTTTGACTGCTGTCTGACGCTACAAGTTCTGGATCTCTCAAACAAT
20 CCTCTCACCGGAGATATTCTGTAAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT
GCCAACACCAAGTTGACTCCCTTCTGTCATCTCCACCGCTCCTATCTCTCTACACCG
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT
GCTGCACCTTCTATTTGCTGTTCCGGCCATTGCACTAGCTTGGTGGCGAAGGAAAAAGCCG
CAGGACCACTTCTTTGATGTACCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACCTG
25 AAGAGGTTTTTCATTGCGTGAAGTACAAGTTGCTTCGGATAATTTTAGCAACAAGAACATA
TTGGGTAGAGGTGGTTTTGGTAAAGTTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG
GCCGTAAAAGGCTAAAAGAGGAGCGCACCCAAGGTGGCGAACTGCAGTTCCAGACAGAG
GTTGAGATGATTAGTATGGCGGTTACAGAAAAGTTGCTTCGGCTTCGTGGATTTTGCATG
ACTCCAACCGAAAGATTGCTTGTTTATCCCTACATGGCTAATGGAAGTGTTCCTCCTGT
30 TTAAGAGAACGTCCCGAGTCCCAGCCACCACTTGATTGGCCAAAGAGACAGCGTATTGCC
TTGGGATCTGCAAGAGGGCTTGCGTATTTACATGATCATTGCGACCCAAAGATTATTCAT
CGAGATGTGAAAGCTGCAAATATTTTGTGGATGAAGAGTTTGAAGCCGTGGTTGGGGAT
TTTGGACTTGCAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCGTGGG
ACAATTGGTCATATAGCCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAAACCGAT
35 GTCTTTGGGTATGGAGTCATGCTTCTTGAGCTTATCACTGGACAAAGGGCTTTTGATCTT
GCTCGCCTCGCGAATGATGATGATGTCATGTTACTAGACTGGGTGAAAGGGTTGTTAAAA
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAAGACGAAGAA
GTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAGTTCACCAATGGAAAGACCC
AAAATGTCTGAAGTTGTAAGAATGCTTGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAG
40 TGGCAAAGGAGGAAATGTTTCAGACAAGATTTCAACTACCCAACCCACCATCCAGCCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA
AGATAAagattcgaaacacgaatgttttttctgtattttgtttttctctgtattttattgag
ggtttttagcttc

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS10 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a
signal sequence. The second domain contains a leucine zipper motif,
containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues,
involved in disulphate bridge formation. The fourth domain contains a
leucine rich repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain contains many
serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain
contains a single transmembrane domain after which the predicted
intracellular domains are positioned. The seventh domain has an
unknown function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth
domain has an unknown function. The last and tenth domain at the C-
terminal end represents part of a single leucine rich repeat,
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL
DLVLRVSGNAEG

DALSALKNSLADP
NKVLQSWDATLVT

35

PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV

M QLGQLPNLQYLELYSNNITGTI

40 PEQLGNLTELVSIDLVLNNLSGPI

PSTLGRLKKLRFLRLNNSLSGEI
PRSLTAVLTLQVLDLSNNPLTGDI
PVNGSFSLTPISFANTK LT PL

5 PASPPPPISPTPPSPAGSNRITG

AIAGGVAAGAAL
LFAVPAIALAWW

10 RRKKPQDHFFDVP AEEDPE
VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGR LAD
GTLVAVKRLKEERTQGGELQFQ

15 TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPESQPPLDWPKRQRIALGSA
RGLAYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMD

20 YK DTHVTTAVRGTTIGHIAPEYL
STGKSSEKTDVFGYGVMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEALVDVDLQGN Y
KDEEVEQLIQVALLCTQSSPME

25 RPKMSEVVRMLE

GDGLAERWEEWQKEEMFRQDFNYPTHH

PAVSGWIIGDSTSQIENEYPSGPR

30

Arabidopsis thaliana RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttgttaacctctcgtactaaaatcttcc**ATGG**TAGTAGTAACAAAGAAGACCATGAAGA
TTCAAATTCATCTCCTTTACTCGTTCTTGTTCTCTGTTTCTCTACTCTCACTCTATCTT
CTGAGCCCAGAAACCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTTGCATGATC
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTTCAGTTGATCCTTGCTAGCTGGGCTATGA
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGCGCCGAGCCAGTCTCTCTCGG
15 GAGGTTTATCTGAGTCTATCGGAAATCTCACAATCTCCGACAAGTGTCATTGCAAAATA
ACAACATCTCCGGCAAATTCACCGGAGCTCGGTTTTCTACCCAAATTACAAACCTTGG
ATCTTTCCAACAACCGATTCTCCGGTGACATCCCTGTTTCCATCGACCAGCTAAGCAGCC
TTCAATATCTGAGACTCAACAACAACCTCTTTGTCTGGGCCCTTCCCTGCTTCTTTGTCCC
AAATTCCTCACCTCTCCTTCTTGGACTTGTCTTACAACAATCTCAGTGGCCCTGTTCTTA
20 AATTCACGCAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTTGTAGAAGCAACCCAC
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT
CAGGACGCAGGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTTGTTA
TACTAGTCCTTGCTCTCGGGTCCTTTTTGTGGTACCGAAAGAAACAAAGAAGGCTACTGA
TCCTTAACTTAAACGCAGATAAACAAGAGGAAGGGCTTCAAGGACTTGGGAATCTAAGAA
25 GCTTCACATTCAGAGAACTCCATGTTTATACAGATGGTTTCAGTTCCAAGAACATTCTCG
GCGCTGGTGGATTTCGGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTACAGTTTCGTATGGAGCTAG
AGATGATTAGCTTAGCTGTTTATAAGAATCTGCTTCGGTTAATTGGTTATTGCGCAACTT
CTGGTGAAAGGCTTCTTGTTTACCCTTACATGCCTAATGGAAGCGTCGCCTCTAAGCTTA
30 AATCTAAACCGGCATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG
GTTTGTGTATCTACATGAGCAATGTGATCCCAAGATCATTCATAGAGATGTAAAGGCAG
CTAATATTCTCTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAAGC
TCCTTAACCATGCGGATTCTCATGTCACAACTGCGGTCCGTGGTACGGTTGGCCACATTG
CACCTGAATATCTCTCCACTGGTCAGTCTTCTGAGAAAACCGATGTGTTTGGGTTCCGGTA
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAACCGTTAGCC
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAAGTAGAGGAAC
TATTGGATCGAGAACTCGGAACCTAAGATAAGATTGAAGTTGGAGAGATGTTGCAAG
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATCGTCCTAAATGTCTGAAGTTGTTT
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCATTCACATT
40 TCTACCATGCCAATATCTCTTCAAGACAATCTCTTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACCTTATCAAATGTTTGGATCTTCGGCTTTTCGATG
ATGACGATGATCATCAGCCTTTAGATTCTTTGCCATGGAACCTATCCGGTCCAAGATAAc
acaatgaaagaaagatatcattttttacgatggatcaaacaatccaatgaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS11 protein.

10 Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
15 leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
20 approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
25 domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
30 domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
interactions.

MVVVTKKTMKIQIHLLYSFLFL
35 CFSTLTLSSEPRNPEV

EALISIRNNLHDP
HGALNNWDEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5 ESIGNLTNLRQVSLQNNNISGKI
 PPELGFLPKLQTLDLSENRFSGDI
 PVSIDQLSSLQYLRNLNNNSLSGPF
 PASLSQIPHLSFLDLSYNNLSGPV
 PKFPARTFNVAGNPLICRSN

10 PPEICSGSINASPL
 SVSLSSSSGRRSNR

 LAIALSVSLGSVVIL
15 VLALGSFCWY

 RKKQRRLLILNLNGADKQEE
 GLQGLGNLRSFTFRELHVYT

20 DGFSSKNILGAGGFGNVYRGKLGD
 GTMVAVKRLKDINGTSGDSQFR
 MELEMISLAVHKNLLRLIGYCA
 TSGERLLVYPMPNGSVASKLK
 SKPALDWNMRKRIAIGAA

25 RGLLYLHEQCDPKI IHRDVKAA
 NILLDECFEAVVGDFGLAKLLN
 HADSHVTTAVRGTVGHIAPEYL
 STGQSSEKTDVFGFGILLLELI
 TGLRALEFGKTVSQKGAMLEW

30 VRKLHEEMKVEELLDRELGTNY
 DKIEVGEMLQVALLCTQYLP AH
 RPKMSEVVLMLE

 GDGLAERWAASHNHSHFYHANI
35 SFKTISSLSTTSVSRLDAHCNDPTYQMFG

 SSAFDDDDHQPLDSFAMELSGPR

Arabidopsis thaliana RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tttaaaaaaccttgctagttctcaattctcatgactttgcttttagtcttagaagtggaaa
ATGGAACATGGATCATCCCGTGGCTTTATTTGGCTGATTCTATTTCTCGATTTTGTTTCC
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA
GGTGACCATACAAACAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA
TGTTTTCATGTTACTTGCAATACTGAAAACAGTGTTACTCGTCTTGACCTGGGGAGTGCT
15 AATCTATCTGGAGAACTGGTGCCACAGCTTGCTCAGCTTCCAAATTTGCAGTACTTGGA
CTTTTTAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGCGACTTGATGGAAC
GTAAGCTTGACCTTTTTTGCAAACAACATAAGCGGTCCCATCCCTTCCTCTCTTGGCAA
CTAGGAAAACCTCCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATTC
TCTTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT
20 ATTCTGTTAATGGTTCCTTTTCGCAGTTCACCTTCTATGAGTTTGGCAATAATAAATTA
AGGCCGCGACCTGCATCTCCTTACCATCACCTTCAGGAACGTCTGCAGCAATAGTAGTG
GGAGTTGCTGCGGGTGACGACTTCTATTTGCGCTTGCTTGGTGGCTGAGAAGAAACTG
CAGGGTCACTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGGTTTATTTAGGACAATTT
AAAAGGTTCTCCTTGCGTGAAGTCTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTA
25 TTGGGCAAAGGACGTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTG
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGGAACAGTTCAGTTTCAAACCGAA
GTTGAGATGATCAGTATGGCCGTTTCATAGGAACCTTGCTTCGGCTTCGTGGCTTTTGCATG
ACTCCAACGAAAGATTACTTGTTTATCCCTACATGGCTAATGGAAGTGTGCTTCTTGT
TTAAGAGAGCGTCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAGAAAGCATATTGCT
30 CTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTGCGACCAAAGATCATTAC
CTGGATGTGAAAGCTGCAAATATACTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGAT
TTTGGGCTAGCAAAATTAATGAATTATAACGACTCCCATGTGACAACTGCTGTACGGGGT
ACGATTGGCCATATAGCGCCCGAGTACCTCTCGACAGGAAAATCTTCTGAGAAGACTGAT
GTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTTCGATCTT
35 GCTCGGCTTGCAAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAA
GAGAAGAAGTTGGAAAGCCTTGTGGATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAA
GTGGAGCAGCTGATACAAATGGCTCTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCA
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAA
TGGCAAAAGGAGGAGATGCCAATACATGATTTTAACTATCAAGCCTATCCTCATGCTGGC
40 ACTGACTGGCTCATCCCCTATTCCAATTCCTTATCGAAAACGATTACCCCTCGGGGCCA

AGATAAaccttttagaaaggggtcatttcttgtgggttcttcaacaagtatatatataggta
gtgaagttgtaagaagcaaaacccacattcacctttgaatatcactactctataa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS12 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 2 leucine residues, each
15 separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
20 contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
25 function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
30 leucine rich repeat, probably involved in protein / protein
interactions.

35

MEHGSSRGFI

WLILFLDFVSRVTGKTQV

DALIALRSSLSSGDHTNNILQ

SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV

5 P QLAQLPNLQYLELFNNNITGEI
PEELGDLMEVLVSLDLFANNISGPI
PSSLGKLGKLRFLRLYNNSLSGEI
PRSLTALP LDVLDISNNRLSGDI
PVNGSFSQFTSMRFA NNLRLPR

10 PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

15 RRKLQGHFLDVPAAEEDPE
VYLGQFKRFSRLRELLVAT

EKFSKRNVLGKGRFGILYKGRAD
DTLVAVKRLNEERTKGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
20 TPTERLLVYPYMANGSVASCLR
ERPEGNPALDWPKRKHIALGSA
RGLAYLHDHCDQKI IHL DVKAA
NILLDEEFEEAVVGDFGLAKLMN
YNDSHVTTAVRG TIGHIAPEYL
25 STGKSSEKTDVFGYGVMLLELI
TGQKAFDLARLANDDDIMLLDW
VKEVLKEKKLESIVDAELEGKY
VETEVEQLIQMALLCTQSSAME
RPKMSEVVRMLE

30 GDGLAERWEEWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR

35

Arabidopsis thaliana RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 taataaacctctaataataatggcctttgcttttactctgatgacaagttcaaaa**ATGGAA**
CAAAGATCACTCCTTTGCTTCCTTTATCTGCTCCTACTATTCAATTTCACTCTCAGAGTC
GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTATCAGGTGAC
CCTGCAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTTACTCCATGTACTTGGTTT
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTTGACCTTGGAATGCAAACTA
TCTGGAAAGTTGGTTCCAGAACTTGGTCAGCTTTTAAACTTGCAGTACTTGGAGCTTTAT
15 AGCAATAACATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGGAAGTAGTAAGC
TTGGATCTTTACGCAAACAGCATAAGCGGTCCCATCCCTTCGTCTCTTGGCAAAGTAGGA
AAACTCCGGTTCTTGCGTCTTAACAACAATAGCTTATCAGGGGAAATTCCAATGACTTTG
ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCTT
GTTAATGGTTCTTTTTCGCTCTTCACTCCTATCAGTTTTCGAATAATAGCTTAACGGAT
20 CTTCCCGAACCTCCGCCTACTTCTACCTCTCCTACGCCACCACCACCTTCAGGGGGGCAA
ATGACTGCAGCAATAGCAGGGGAGTTGCTGCAGGTGCAGCACTTCTATTTGCTGTTCCA
GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAACACAGGACCACTTTTTTGATGTACCT
GCTGAAGAAGACCCAGAGGTTCAATTTAGGACAACCTCAAAGGTTTACCTTGCGTGAAGTG
TTAGTTGCTACTGATAACTTTAGCAATAAAAATGTATTGGGTAGAGGTGGTTTTGGTAAA
25 GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAAAAGAAGAA
CGTACCAAGGGTGGGGAACTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT
CATAGGAACCTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAAGTAAAGATTACTTGT
TATCCCTACATGGCTAATGGAAGTGTGCTTCTTGTTTAAGAGAGCGTCCTGAAGGCAAT
CCAGCACTTGATTGGCCAAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGCG
30 TATTTACATGATCATTGCGACCAAAAAATCATTACCGGGATGTTAAAGCTGCTAATATA
TTGTTAGATGAAGAGTTTGAAGCTGTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT
TATAATGACTCCCATGTGACAACCTGCTGTACGCGGTACAATTGGCCATATAGCGCCCGAG
TACCTCTCGACAGGAAAATCTTCTGAGAAGACTGATGTTTTTGGGTACGGGGTCATGCTT
CTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTTGCTCGGCTTGCAAATGATGATGAT
35 ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAAGCCTTG
GATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAAGTGGAGCAGCTGATACAAATGGCT
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCAAAGATGTCAGAAGTAGTGAGAATG
CTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAATGGCAAAGGAGGAGATGCCAATA
CATGATTTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCCTATTCC
40 AATTCCTTATCGAAAACGATTACCCCTCGGGTCCAAGATAAccttttagaaagggctctt

ttcttgtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa
aa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS13 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

10

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains
leucine zipper motifs, containing 2 times 2 leucine residues,
each separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
interactions.

30

MEQRSLLCFLYLL
LLFNFTLRVAGNAEG

35

DALTQLKNSLSSGDP
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV
P ELGQLLNLYLELYSNNITGEI
PEELGDLVELVSLDLYANSISGPI
5 PSSLGKLGKLRFLRLNNSLSGEI
PMTLTSVQLQV LDISNNRLSGDI
PVNGSFSLFTPISFANNSLTDLPE

PPPTSTSPTPPPPSG
10 GQMTAAIAGGVAAGAAL
LFAVPAIAFAWWL

RRKPQDHFFDVPGAEDPE
15 VHLGQLKRFTLRELLVAT

DNFSNKNVLGRGGFGKVYKGR LAD
GNLVAVKRLKEERTKGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
20 TPTERLLVYPYMANGSVASCLR
ERPEGNPALDWPKRKHIALGSA
RGLAYLHDHCDQKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMN
YNDSHVTTAVRGTIGHIAPEYL
25 STGKSSEKTDVFGYGVMLLELI
TGQKAFDLARLANDDDIMLLDW
VKEVLKEKKLES LVD AELEGKY
VETEVEQLIQMALLCTQSSAME
RPKMSEVVRMLE
30 GDGLAERWEEWQKEEMPIHDFNYQA

YPHAGTDWLIPYSNSLIENDYPSGPR
35

Arabidopsis thaliana RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctgcaccttagagattaataactctcaagaaaaacaagttttgattcggacaaag**ATG**TTG
CAAGGAAGAAGAGAAGCAAAAAAGAGTTATGCTTTGTTCTCTTCAACTTTCTTCTTCTTC
TTTATCTGTTTTCTTTCTTCTTCTTCTGCGAAGTCTACAGACAAAGTTGTTGCCTTAATA
GGAATCAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA
GTTGATCCATGTAGCTGGAACATGATCACTTGTCTGATGGTTTTGTCATAAGGCTAGAA
15 GCTCCAAGCCAAAACCTTATCAGGAACCTTTTCATCAAGTATTGGAAATTTAACAATCTT
CAAACGTATACAGGTTATTGCAGAACAAATTACATAACAGGAAACATCCCTCATGAGATT
GGGAAATTGATGAAACTCAAAACACTTGATCTCTCTACCAATAACTTCACTGGTCAAATC
CCATTCACTCTTTCTTACTCCAAAATCTTCACAGGAGGGTTAATAATAACAGCCTGACA
GGAACAATTCCTAGCTCATTGGCAAACATGACCCAACTCACTTTTTTGGATTTGTCGTAT
20 AATAACTTGAGTGGACCAGTTCCAAGATCACTTGCCAAAACATTCAATGTTATGGGCAAT
TCTCAGATTTGTCCAACAGGAAGTGAAGAACTGTAATGGGACTCAGCCTAAGCCAATG
TCAATCACCTTGAACAGTTCTCAAAGAACTAAAAACCGGAAATCGCGGTAGTCTTCGGT
GTAAGCTTGACATGTGTTGCTTGTGATCATTGGCTTTGGTTTTCTTCTTTGGTGGAGA
AGAAGACATAACAAACAAGTATTATCTTTGACATTAATGAGCAAAACAAGGAAGAAATG
25 TGTCTAGGGAATCTAAGGAGGTTTAATTTCAAAGAACTTCAATCCGCAACTAGTAACCTC
AGCAGCAAGAATCTGGTCGGAAAAGGAGGGTTTGGAAATGTGTATAAAGGTTGTCTTCAT
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT
CAGTTTCAGACAGAGCTTGAAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA
TACGGTTTTCTGTACTACTTCCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAATGGC
30 AGTGTGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGGCACAAGAAAGCGAATA
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTTGCATGAGCAATGTGATCCAAAGATCATT
CACCGTGATGTCAAAGCTGCGAACATACTTCTTGACGATTACTTTGAAGCTGTTGTCTGGA
GATTTCTGGGTTGGCTAAGCTTTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA
GGAACAGTGGGTACATTGCACCTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA
35 GATGTGTTCTGGTTTTCTGGGATTCTTCTTCTCGAATTGATTACTGGATTGAGAGCTCTTGAA
TTCGGAAAAGCAGCAAACCAAAGAGGAGCGATACTTGATTGGGTAAAGAACTACAACAA
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTTGAAGAGCAACTACGATAGAATAGAA
GTGGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCCATTCACCGTCCT
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGGCGATGGTCTTGTGAGAAATGGGAAGCT
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTTCTTCTCTCT

GAACGTTATTTCGGATCTTACAGATGATTCTCGGTGCTGGTTCAAGCCATGGAGTTATCA
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS14 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
15 contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
20 contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
25 protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
30 interactions.

MLQGRREAKKSYALEFSSTFF
FFFICFLSSSSAELTDKV

35 VALIGIKSSLTDP
HGVLMNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS
SIGNLTNLQTVYRLLQNNYITGNI
PHEIGKLMKLTLDLSTNNFTGQI
5 PFTLSYSKNLHRRV NNNSLTGTI
PSSLANMTQLTFLDLSYNNLSGPV
PRSLAKTFNVMGNSQICPT

GTEKDCNGTQPKPMSITLNSSQR
10 TKNRK

IAVVFGVSLTCVCLLIIGFGFLLWW

RRRHNKQVLFFDINEQNKE
15 EMCLGNLRRFNFKEQSAT

SNFSSKNLVGKGGFGNVYKGCLHD
GSIIAVKRLKDINNGGGEVQFQ
TELEMISLAVHRNLLRLYGECT
20 TSSERLLVYPYMSNGSVA
SRLKAKPVLWDGTRKRIALGAG
RGLLYLHEQCDPKIIHRDVKAA
NILLDDYFEAVVGDFGLAKLLD
HEESHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGLRALEFGKAANQRGAILDW
VKKLQQEKKLEQIVDKDLKSNY
DRIEVEEMVQVALLCTQYLPPIH
RPKMSEVVRMLE
30
GDGLVEKWEASSQRAET
NRSYSKPNEFSSS

ERYSDLTDDSSVLVQAMELSGPR
35

Legends

Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in
10 targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein
15 protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and
20 Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane
25 domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain
30 with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

35 Alagntment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

5 Intron-Exon boundaries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

20 Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects.

25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which

35 the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

Figure 9

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

Figure 10.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GASA3 gene in sense direction, i.e. overexpressing GASA3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25 Figure 12

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense
30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified). Epidermal cell size is not changed in transgenic plants compared with the control.

Figure 14

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermis of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

Figure 15

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

5 Figure 17

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems
10 from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1,
15 CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants
20 are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single
25 transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 Figure 19

Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation
35 could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show
5 the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

Figure 24

10 Average root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

Figure 25

T3 seedlings are shown from a strong co-suppressing RKS10
15 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

20

Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of
representative examples of the lateral root development from
25 transgenic RKS and ELS transgenic roots.

Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken
30 under same magnification.

Figure 28

Arabidopsis thaliana WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation
35 of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems.

The generative shoots are photographed with similar magnification.

Figure 29

Arabidopsis thaliana WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined
5 flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this
10 structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

15 Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem
20 produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be
25 observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis*
30 plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a
35 terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

Detailed description

1.Modifying organ size

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

- the size of plant organs
- the growth rate
- the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:

- the size of plant organs

the growth rate
the total plant size

5

Results obtained (see also figures 6 to 13)

Overexpression and antisense constructs of full length RKS
cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis*
10 *thaliana* and in *Nicotiana tabacum*. Subsequent generations of
stably transformed plants were investigated for phenotypes and
analyzed in detail. The phenotype observed in transgenic
plants with antisense constructs of RKS4 (GT-RKS4-a) could be
described as dwarf plants in which all plant organs showed a
15 decrease in organs size and growth rate. Overexpression of
RKS4 (GT-RKS4-s) resulted in plants with increased size of
organs and an increase in growth rate. Since cell size alone
was not responsible for the modifications in organ size of
petals it can be concluded that RKS4 is involved in the
20 regulation of the cellular divisions during plant growth and
organ formation. Overexpression of RKS 4 results in an
increase of cellular divisions whereas a decrease in
endogenous RKS 4 gene product levels within the plant results
in a decrease of cellular division rates.

25

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2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

30 Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:
the size of plant organs
the growth rate
the yield of harvested crop
the yield of total plant material
the total plant size

Decreasing the levels of endogenous RKS signaling complex members in order to decrease:

the size of plant organs

5 the growth rate

the total plant size

Results obtained

Overexpression and antisense constructs of full length RKS
10 cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.

15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division. Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10
20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding
25 cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants, no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within
30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.

Normal RKS10 function also involves an activation process on
35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

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3. Regeneration

Modification the levels of different RKS and ELS genes within
5 plants allows the initiation and / or outgrowth of apical
meristems, resulting in the formation of large numbers of
plantlets from a single source. A number of gene products that
is able to increase the regeneration potential of plants is
known already. Examples of these are KNAT1, cycD3, CUC2 and
10 IPT. Here we show that modulation of the endogenous levels of
RKS genes results in the formation of new shoots and plantlets
in different plant species like *Nicotiana tabacum* and
Arabidopsis thaliana. herewith the invention provides a method
for modulating a developmental pathway of a plant or plant
15 cell comprising modifying a gene or modifying expression of
said gene, wherein said gene is encoding a protein belonging
to a signaling complex comprising RKS protein, ELS protein,
NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein,
allowing modulating apical meristem formation, in particular
20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or
RKS10 gene or functional equivalent thereof. A direct
application of a method according to the invention is the
stable or transient expression of RKS and ELS genes or gene
products in order to initiate vegetative reproduction.
25 Regeneration can be induced after overexpression of for
example RKS0 and ELS1; or by co-suppression of for example the
endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or
co-suppression of these RKS and ELS gene products can be
either transient, or stable by integration of the
30 corresponding expression cassettes in the plant genome.

Results obtained

Overexpression and antisense constructs of full length RKS and
ELS cDNA clones have been made under the control of 35S
35 promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

Literature

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4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

Results obtained

- 5 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector (pGreen5K) were tested for their ability to induce fasciation (Overexpression constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in
- 15 fasciated plants, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only positive results are shown). Antisense constructs of RKS3 gave also rise to fasciation (Figure 19).

20

Literature

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5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased.

Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products.

Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by

overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or
5 ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be
10 influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

Results obtained

15 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
20 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root
25 development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown
30 together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

35

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6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression
5 results in an extremely bushy phenotype.

Results obtained

Changing the normal levels of endogenous RKS10 within the
10 plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were
15 normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in
20 RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem
25 develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a
30 number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a
35 petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together with other phenotypes (results not shown).

Literature

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7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

30 Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

Literature

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8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

15 **At2g27080;**
 MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ
 LSRKKTNRSN CRCCFCFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN
 STSPISPSFN VTVRSRNGNG KIGVYYEKES SVDVYYNDVD ISNGVMPVFY QPAKNVTVVK
 LVLGSKIQL TSGMRKEMRN EVSKTVPFK LKIKAPVKIK FGSVKTWTMI VNVDCDVTVD
 20 KLTAPSRIVS RKCSHDVDLW **

At5g21130
 MTVEKPQEMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGPPPGTYVI
 KLPKDQIYRV PPPENAHRYE YLSRRKTNKS
 25 CCRRCLCYSL SALLIIIVLA AIAFGFFYL
 YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGLIYEKG NEADVFFNGT
 KLGNGEFTAF KQPAGNVTVI VTVLKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF
 KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL L*

30 **At1g65690**
 MSQHQKIYPV QDPEAATARP TAPLVPRGSS RSEHGDPKSV PLNQRQRFV PLAPPKRRS
 CCCRCFCYTF CFLLLLVLVAV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTAF
 NVTITAKNPN EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI YVEMTGQTQN
 ASGLRTTLEE QQORTGNIPL RIRVNQPVV KFGKCLKFEV RFLVRCGVFV DSLATNNVIK
 35 IQSSSCKFRL RL*

At5g36970
 MSDHQKIHPV SDPEAPPHT APLVPRGSSR SEHGDPKTQ QAAPLDPPRE KKGSR
 CWCRCVCYTLLVLF LLIVIVGAIV GILYLVFRPK FPDYNIDRLQ LTRFQLNQDL
 40 SLSTAFNVTI
 TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTIIILVEM TGFTQNATSL
 MTTLQEQQL TGSIPLRIRV TQPVRIKLG LKLMKVRFLV RCGVSVDSL ANSVIRVRSS
 NCKYRFRL*

45 **At1g54540**
 MGDQQKIHPV LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL
 LVIALIALAI AVAVVYFVFH PKLPSYEVNS LRVTNLGINL DLSLSAEFKV EITARNPNEK
 IGIYYEKGGH IGVWYDKTKL CEGPIPRFYQ GHRNVTKLNV ALTGRAQYGN TVLAALQQQ
 QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL STNNNINIK SDCSFKAKL*
 50

At5g06320

MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG
 IAALIIWLIF RPNALFKHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYYDEIE
 VRGYYGDQRF GMSNNISKFY QGHKNTTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI
 DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F**

5

At5g11890

MTDRVFPASK PPTATNGAPP VGSIPPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP
 QPYSRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFSVPSI
 RISRVNLTTT SDSSVSHLSS FFNFTLISEN PNQHLFSFSYD PFTVTVNSAK SGTMLGNGTV
 PAFFSDNGNK TSFHGVIATS TAARELDPDE AKHLRSDLTR ARVGYEIEMR TKVKMIMGKL
 KSEGVEIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLSV KVKWWSF*

10

At1g17620

MTDDRVPASP KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG
 CCCRCCCWTIFVII LLLLIVAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV
 RLTTAISLSV
 IARNPNKNVG FIYDVTDITL YKASTGGDDD VVIGKGTIAA FSHGKKNNTT LRSTIGSPPD
 ELDEISAGKL KGDLLAKKAV AIKIVLNSKV KVKMGALKTP KSGIRVTCEG IKVVAPTGGK
 ATTATTSAAK CKVDPRFKIW KITF**

15

20

At3g11650

MGSKQPYLNG AYYGPSIPPP PKAHRSYNSP GFGCCCFSCS GSCLRCCGCC ILSLICNILI
 AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDPNN NLHYSDDLNF TIRNPNQRVG
 VYYDEFSVSG YYGDQRFQSA NVSSFYQGHK NTTVILTKE GQNLVVLGDG ARTDLKDEK
 SGIYRINAKL RLSVRFKFWF IKSWKLKPKI KCDDLKIPLG SSNSTGGFKF QPVQCFDLS**

25

At2g22180

MEGPRRPPSA TAPDSDDDKP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL
 PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL
 LWFFIILVIF GFLLGAILLI LHFAFNPTLP VFAVERLTVN PSNFEVTLRA ENPTSNMGVR
 YMMEKNGVVS LTYKNKSLGS GKFPGLSQAA SGSDKVNKL NGSTKNAVVO PRGSKQPVVL
 MLNMELKAEY EAGPVKRNKE VVVTCDVKVK GLLDKAKVEI VSENCESEFK N*

30

At5g22870

MCHKPKLELM PMETSPAQPL RRPSLICIFY LVILTILFMA AVGFLITWLE TKPKKLRYTV
 ENASVQNFNL TNDNHMSATF QFTIQSHNPN HRISVYYSSV EIFVKFKDQT LAFDTVEPFH
 QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRFK VGIWKSSHRT
 AKIKCSHVTV SLSQPNKSQN SSCDADI*

35

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At2g35980

MAAEQPLNGA FYGPSVPPPA PKGYYYRRGHG RGCGCCLLSL FVKVIISLIV ILGVAALIFW
 LIVRPRAIKF HVTDAALTRF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEHAHAYYE
 GKRFSTITLT PFYQGHKNTT VLTPTFQGN LVIFNAGQSR TLNAERISGV YNIEIKFRLR
 VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTTSTVFP IKCDFDF**

45

At2g46300

MADYQMNPLV QKPPGYRDPN MSSPPPPPPP IQQQPMRKAV PMPTSYPKK KRRSCCRFCC
 CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLASFRLD GFKLADDPDG ASLSATAVAR
 VEMKNPNKSL VFYYGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL
 VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCGGVS LNKLDTDSPK
 CILNTLKWKY IISN*

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At4g05220

MTPDRTTIPI RTSPVPRAQP MKRHHSASY AHRVRESLST RISKFICAMF
 LLLVFFVGVF AFILWLSLRP HRPRFHIQDF

55

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSMEGSI YYKDQRVGLI
 PLLNPFQQP TTTTIVTGTI TGASLTVNSN RWTEFSNDRA QGTVGFRLDI
 VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHKK CPVYFT*

5 **At2g35460**

MANGLNGASY GPPIKPPVKT YYSHGRRGSD VGCGICGCFS SCLCCGGCL VNIICNIIIG
 VLVCLGVVAL ILWFILRPV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG
 IHYDQLEVRG YYGDQRFSA NMTSFYQGHK NTTVVGTEN GQKLVLGAG GRRDFREDRR
 SGVYRIDVKL RFKLRFKFGF LNSWAVRPKI KCHLKVPLST SSSDERFQFH PTKCHVDL*

10

At2g27260

MQDPSRPATG YPYPPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR
 RLFIVFTTFL LLLGLILFIF FLIVRPQLPD VNLNSLSVSN FNVSNQVSG KWDILQLQFRN
 PNSKMSLHYE TALCAMYNR VSLSETRLQP FDQKKDQTV VNATLSVSGT YVDGRLVDSI
 GKERSVKGNV EFDLRMISYV TFRYGAFFFF RYVTVYCDDV AVGVVPVSSGE GKMGVSSKRC
 KTY**

15

At4g01410

MGEGEAKAEH AAKADHKNAP SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIIAL
 ILWLVRPHK PRLTVGAAI YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT
 YKQIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNDEAY GVVLMRVVIF
 GRLRWKAGAI KTGRYGFYAR CDVWLRFNPS SNGQVPLLAP STCKVDV*

20

At5g22200

MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTI
 NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGH
 EVTVWSPFLI GSAVPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHVN
 CPAFITVTGK LTGTGPAIKY QLVQRCADV *

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At1g61760

MHNKVDLSLV RSNPSTRPIS RHHSASNIVH RVKESLTTRV SKLCAIFLS LLLCLGIITF
 ILWISLQPHR PRVHIRGFSI SGLSRPDGFE TSHISFKITA HNPQNQVGIY YDSMEGVSYY
 KEKRIGSTKL TNPFIYQDPKN TSSIDGALS PAMAVNKDRW MEMERDRNQ KIMFRLKVRS
 MIRFKVYTW HSKSHMYASC YIEIGWDGML LSATKDKRCP VYFT*

30

35

At3g52470

MSKDCGNHGG GKEVVVRKLC AAIIFIVIV LITIFLVWVI LRPTKPRFVL QDATVYAFNL
 SQPNLLTSNF QVTIASRNP SKIGIYYDRL HVIATYMNQQ ITLRTAIPPT YQGHKEVNVW
 SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRTLITGKY HIHVRCAFI
 NLGNKAAGVL VGDNAVKYTL ANKCSVNV**

40

At5g53730

MSQISITSPK HCAKKGGINI NNRHKKLFFT FSTFFSGLLL IIFLVWLILH PERPEFSLTE
 ADIYSLNLT STHLLNSSV QLTFLSKNPN KKVGIYYDKL LVYAAYRGQQ ITSEASLPPF
 YQSHEEINLL TAFLOGTLP VAQSFYQIS RERSTGKIII GMKMDGKLRW KIGTWVSGAY
 RFNVNCLAIV AFGMNMTTP LASLQGTCS TTI*

45

At4g01110

MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSSMLRR PPKHAIPAAF YPTKKRQWSR
 CRVFCCCVCI TVAIVILLI LTVSVFFLYY SPRLPVVRLS SFRVSNFNFS GKGAGDGLSQ
 LTAEATARLD FRNPNGKLR YGYNVDVAVS VGEDDFETSL GSTKVKGFE KPGNRTVVIV
 PIKVKKQQVD DPTVKRLRAD MKSKKLVVKV MAKTKVGLGV GRRKIVTVGV TISCGGVRLQ
 TLDSKMSKCT IKMLKWYVPI QVKCI*

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At2g35960

MTTKDCGNHG GGGGGGTASR ICGVIIGFII IVLITIFLVW IILQPTKPRF ILQDATVYAF

55

NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVVYATYRN QQITLRTAIP PTYQGHKEDN
 VWSPFVYGNS VPIAPFNAVA LGDEQNRGFV TLIIRADGRV RWKVGTITG KYHLHVRCQA
 FINLADKAAG VHVGENAVKY MLINKCSNVN *

5 **At3g52460**

MPSPPEEETQ PKPDTGPGQN SERDINQPPP PPPQSQPPPP QTQQQTYPPV MGYPGYHQPP
 PPYPNYPNAP YQYYPYAQAP PASYYGSSYP AQONPVIYQRP ASSGFVRGIF TGLIVLVVLL
 CISTTITWLTV LRPQIPLFSV NNFSVSNFNV TGPVFSQWT ANLTIENQNT KLKGYFDRIQ
 GLVYHQNAVG EDEFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMCKERE

10 TGTVTFSLRM AVWVTFKTDG WAARESGLV FCGKLVGFE GISGNGAVLL PKPLPCVVVY*

At4g09590

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV WIILQPKNPE FILQDTTVYA
 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKED
 15 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTITI GNYHLHVRCQ
 AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At2g35970

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPE FILQDTTVYA
 20 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKEN
 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGTITI GNYHLHVRCQ
 AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At3g26350

25 MSHHHHHETN PHFARIPSON PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHPVA
 PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPKRKT QNSSKRPLLL SPEDNQQRQ
 PPPQAPQRNG GGYGSTLPPI PKPSPWRTAP TSPPHRRGP RLPPPSRETN AMTWSAAFCC
 AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAAYL DMGFLLNGDL TILANVTNPS
 KKSSVEFSYV TFELYYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR
 30 QIETGPVLLN LRGMFHARSH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTKR*

At3g11660

MKDCENHGHG RRKLIRRIFW SIIFVLFIIF LTILLIWAII QPSKPRFILQ DATVYAFNVS
 GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI
 35 WSPFVYGTSTV PIAPFNGVSL DTDKDNQVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY
 INFGNKANGV IVGDNAVKYT FTTSCSVSV**

At3g44220

MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFVVFLVWA ILHPHGPRFV
 40 LQDATIYAFN VSQPNYLTSN LQVTLSSRNP NDKIGIFYDR LDIYASYRNQ
 QVTLATLLPA TYQGHLDVTI WSPFLYGTIV PVAPYFSPAL SQDLTAGMVL
 LNIKIDGWVR WKVGTWVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV*

At1g08160

45 MVPPNPAHQP ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL
 TLRPKRLIYT VEAASVQEFA IGNNDDHINA KFSYVIKSYN PEKHVSVRYH SMRISTAHN
 QSAHKNISP FKQRPKNETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS
 YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQRVLCCTR L**

50 **At2g01080**

MPPPPSSSRA GLNGDPIAAQ NQQPYRSYS SSSASLKGK CCCLFLLFAF LALLVLAVVL
 IVILAVKPKK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG
 ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAHAADL VRDASLNDRV
 ELTVRGDVGK KIRVMNFDSP GVQVLLPSFL PAFCSLSDLA *

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At5g06330

MTSKDCGSHD SHSSCNRKIV IWTISIILL ILVVILLVWA ILQPSKPRFV LQDATVFNFN
 VSGNPPNLLT SNFQFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSPM LTTYQGHKEV
 NVWSPFVGGY SVPVAPYNAF YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLHVRCH
 ALINFGSSAA GVIVGKYMLT ETCVSVSV*

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At5g56050

MSKFSPPPQS QPQPPETPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK
 SPLSNQKSPA TPKLDSMEAH PLHETMVLLQ LRTSRTNPWI WCGAALCFIF SILLIVFGIA
 TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTNPNKKL NVRFENLMVE
 10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRRQVT SNRIAYEIRS
 NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW*

At3g20600**NDR1**

15 MNNQNEDETEG GRNCCTCCLS FIFTAGLTSL FLWLSLRADK PKCSIQNFFI PALGKDPNSR
 DNTTLNFMVR CDNPKNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNYTV PKFYQGHKKK
 AKKWGQVKPL NNQTVLRAVL PNGSAVFRD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD
 GVKAQKKGIK MKKSDSSFPL RSSFPISVLM NLLVFFAIR*

20 **At3g54200**

MSDFSIPKDD KKEEEKPATA MLPPPKPNAS SMETQSANTG TAKKLRRKRN CKICICFTIL
 LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLQASVNP LLLKVLLNLT LNVDSLKNP
 NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMDRL LSETQLLSDV
 MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLISISVS DRNVT SQHCK YSTKL*

25

At3g20590

non-race specific disease resistance protein, putative

MTKIDPEEEL GRKCCTCFK FIFTTRLGAL ILWLSLRACK PKCSIQNFYI PALSKNLSSR
 DNTTLNFMVR CDNPKNKDKGI YYDDVHLTFS TINTTTTNSS DLVLVANYTV PKFYQGHKKK
 30 AKKWGQVWPL NNQTVLRAVL PNGSAVFRD LKTHVRFKIV FWKTKWYRRI KVGADVEVNG
 DGVKAQKKGS KTKKSDSSLP LRSSFPIFVL MNLLVFFAIR *

At4g39740

MSHVTATSLA RFTKPVPKPA SSPIVNTKLT TSGGRTAAFM DLSSFRLTVW
 35 DPDTANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMITIT
 EMNNQMHRL EQLLLFLPGS LFLRLSTILH YPGEGRNRPD PLEHALRRSR
 SLGLDQEEAA KKVIRVGRDS KNDYVNVVEN QAASFLRRCG PSKRIQSVNY
 CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH
 YNDERRAVPR GQASSNSGCG CGSNTTVKGP IIGGPFTLVS TENKIVTEND
 40 FCGKWVLLYF GYSFSPDVGP EQLKMMKAV DKLAILLNPL TFGCLYLYAE
 FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVDT SHNMYLINPK
 MEIVRCFGVE YNPDELSQEL LKEVASVSQ*

At1g32270 syntaxin, putative

45 MVRSDNVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR
 FEATVYYMNQ RLGA VPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF
 EDDQKTGVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS
 TGGHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA
 ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QEQRVLMESR
 50 RQEIVLLDNE ISLNEARIEA REQGIQEVKH QISEVMEFEMK DLAVMVDHQG
 TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLLFLLSG
 DLCRCVCVGS ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK
 KVNKPNGFVF CVLGHK*

55 **At1g13050**

MSHHHYETNP HFVQFSLQDQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP
 PETIHESPSS RPLPLRPEEP LPPRHNPNSA RPLQLSPREEQ RPPHRGYGSE PTPWRRAPTR
 PAYQQGPKRT KPMTLPATIC CAILLIVLIL SGLILLLVYL ANRPRSPYFD ISAATLNTAN
 5 LDMGYVLNGD LAVVVNFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMFT
 SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL
 NTPPAGTMRA RRCNTRK*

At5g45320

10 MPRLTSRHGT SPFIWCAAI CAIISIVVIV GGIIIVFVGYL VIHPRVPIIS
 VADAHLDLFLK YDIVGVLTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK
 PIAILKAPEF EVVKEKSMFL PYLVQSYPIP LNPTMMQAVD YAVKKDVITF
 ELKGGSRTRW RVGPLGSVKF ECNLSCQLRF RPSDHSYIPS PCTSAHKH*

At3g20610

15 MDRDDAWEF VTIVGSLMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSLISS
 DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLV ANYTVPRFYQ GHEKKAKKWG
 QALPFNNQTV IQAVLPNGSA IFRVDLKMV KYKVMWSWTK RYKLKASVNL EVNEDGATKV
 KDKEDGIKMK ISDSSPQRLT FFQVCFSIIC VLMNWLIFLA IR*

At4g26490

20 MVLTKPATVR ENGLDAEPRK DRVILRQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL
 HTIYFDTPEF FNGDLSMLVN FTNPNKKIEV KFEKLRIELF FFNRLIAAQV VQPFLQKKHE
 TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGTF KVKAHFGMIH YSYQLHGRCQ
 25 LQMTGPPTGI LISRNCTTKK *

At5g42860

30 MHAKTDEVT SLSASSPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV
 LTSPMGSPPH SHSSSRFSK INSKRKSHA GEKQFAMIEE EGLLDDGDRE
 QEALPRRCYV LAFIVGFSL FAFSLILYA AAKPQPKIS VKSITFEQLK
 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSSP IDLSFSQITI
 GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK
 KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLGKLVQPKF YKRIVCLINF
 EHKKLSKHIP ITNNCTVTSI *

At1g45688

35 MHAKTDEVT SLAASSPARS PRRPVYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPPHS
 HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHGG EKQWKECAVI EEGLLDDGD
 RDGGVPRRCY VLAFIGVFFI LFGFFSLILY GAAKPMKPKI TVKSITFETL KIAGQDAGG
 VGTDMITMNA TLRMLYRNTG TFFGVHVTST PIDLSFSQIK IGSQSVKKFY QGRKSERTVL
 40 VHVIGEKIPL YGSGSTLLPP APPAPLPKP KKKGAPVPI DPAPPAPVP MTLSEVVRSR
 AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV*

At4g26820

45 MDDEQNLVEE MNQQLLITVI DTEKVPRLP ISSRSHQESE PANISHWSLL FKLFLAITIM
 GACVAGVTFV ILITPTPPTV HVQSMHISFA NHNLPVWSAT FSIKNPNEKL HVTYENPSVW
 LVHRGKLVST ARADSFQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGLDMV
 FSGRVGFYPG TSALWGEQYM SAVCENVSAL LYNVDDEIYG TNRSVLSFDG RLVCSVRLPK
 YP*

50

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.

- 10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.
- 15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.
- 20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).
- 30 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5 Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898.)

Further references

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Claims

1. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying
5 expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein or encoding a protein comprising a ligand for said complex.
10
2. A method according to claim 1 allowing modulating cellular division during plant growth or organ formation
3. A method according to claim 2 wherein said gene comprises
15 an RKS4 or RKS10 gene or functional equivalent thereof.
4. A method according to claim 1 allowing modulating apical meristem formation.
- 20 5. A method according to claim 4 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof.
6. A method according to claim 4 allowing modulating
25 fasciation.
7. A method according to claim 6 wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof.
30
8. A method according to claim 4 allowing modulating root development.
9. A method according to claim 7 wherein said gene comprises
35 an ELS1, ELS 2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

10. A method according to claim 4 allowing modulating meristem identity.

11. A method according to claim 9 wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof.

12. A method according to claim 1 allowing modulating pollen development.

10

13. A method according to claim 11 wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

14. A method for providing resistance to a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising NDR/NHL protein, or encoding a protein comprising a ligand for said complex.

20

15. A method for obtaining a plant or plant cell with a modulated development comprising subjecting a plant or plant cell to a method according to anyone of claims 1 to 13.

16. A method for obtaining a resistant plant or plant cell comprising subjecting a plant or plant cell to a method according to claim 14.

17. A plant or plant cell obtainable with a method according to claim 15 or 16.

30

Fig. 1

Different domains of RKS proteins

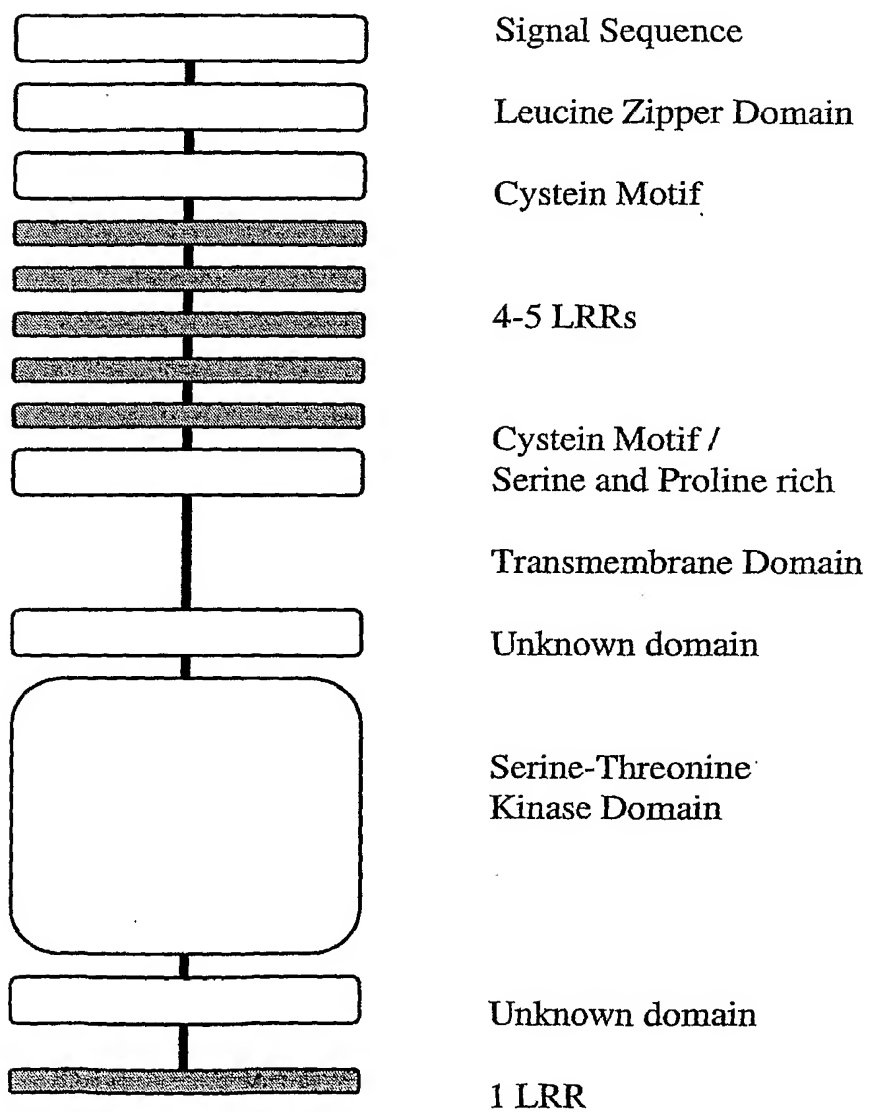


Fig. 2

Developmental tree of the different Receptor Kinases like SERK (RKS) genes.

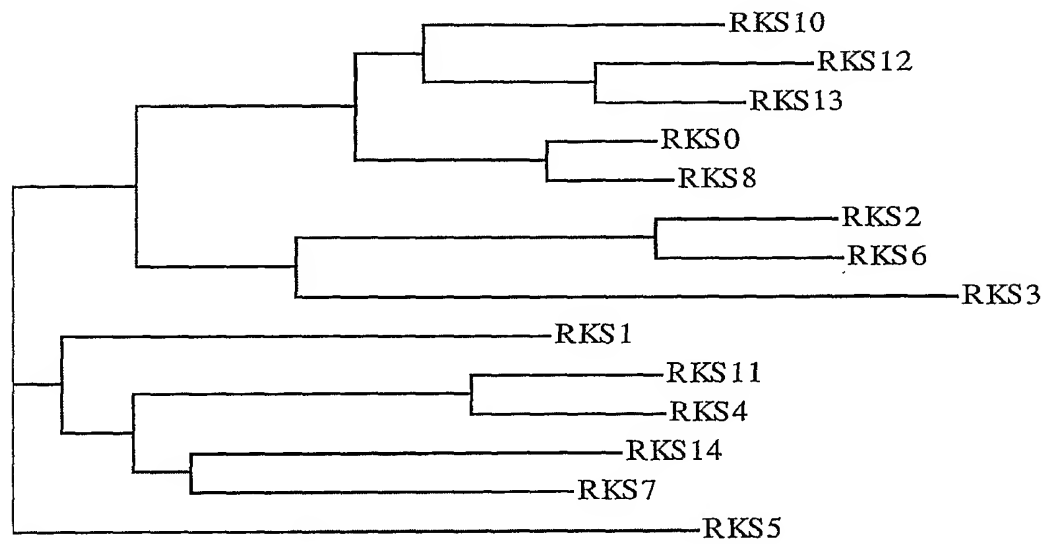
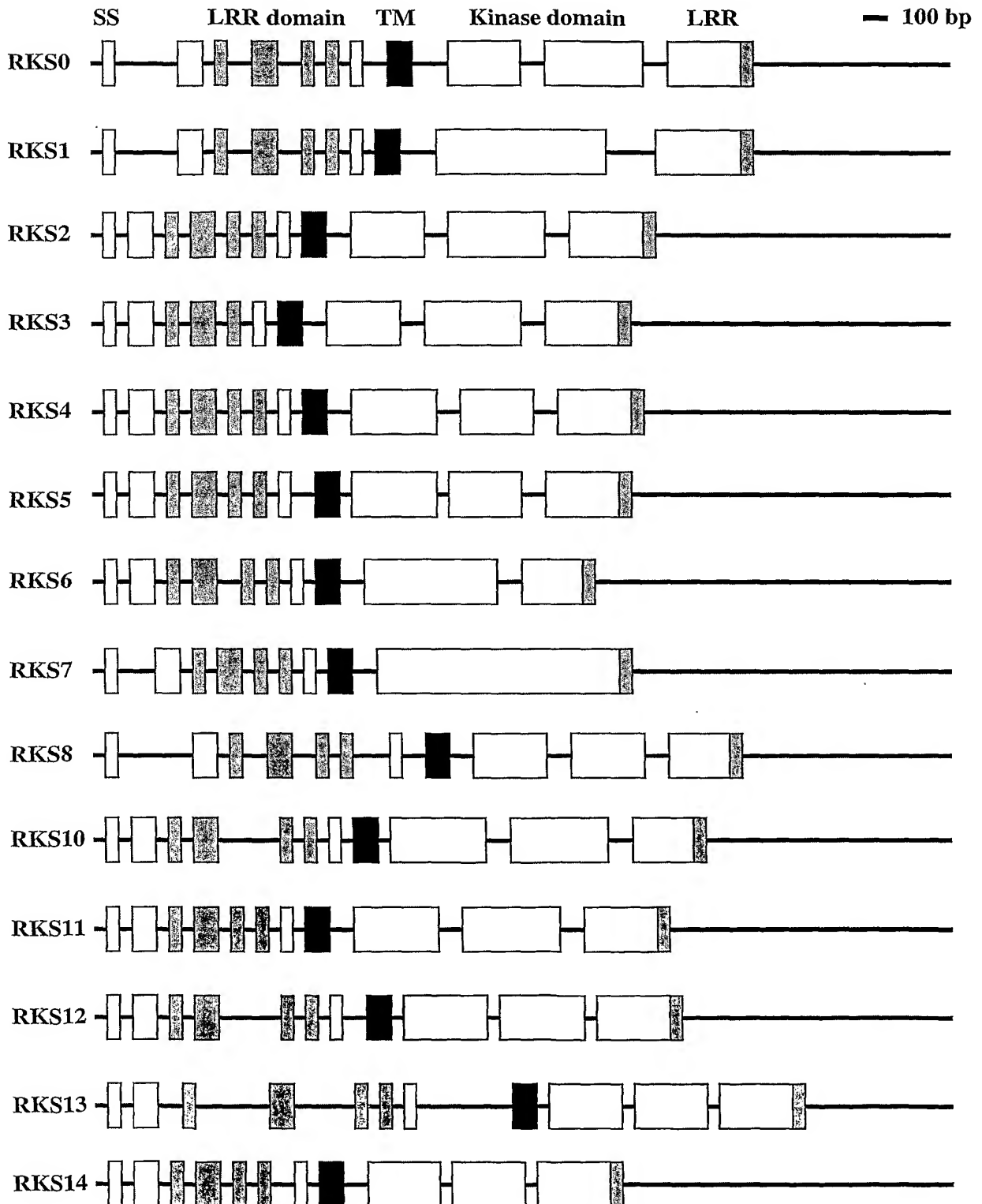


Fig. 3

Intron-Exon structure of the RKS genes in *Arabidopsis thaliana* var. Columbia.
SS signal sequence; LRR leucine rich repeat domain; TM transmembrane domain.



Chromosomal location of RKS genes
in *Arabidopsis thaliana*

I II III IV V

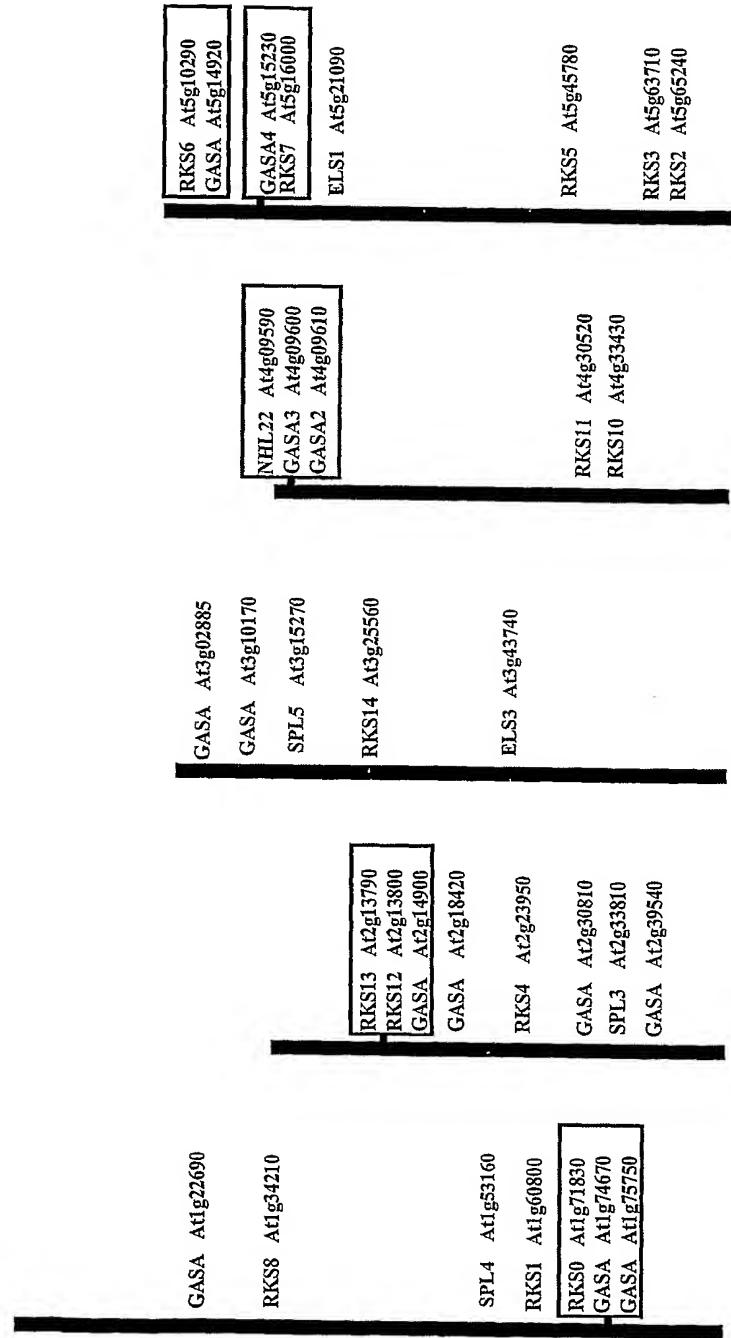


Fig. 4

RKS-mediated signal transduction pathway in plants

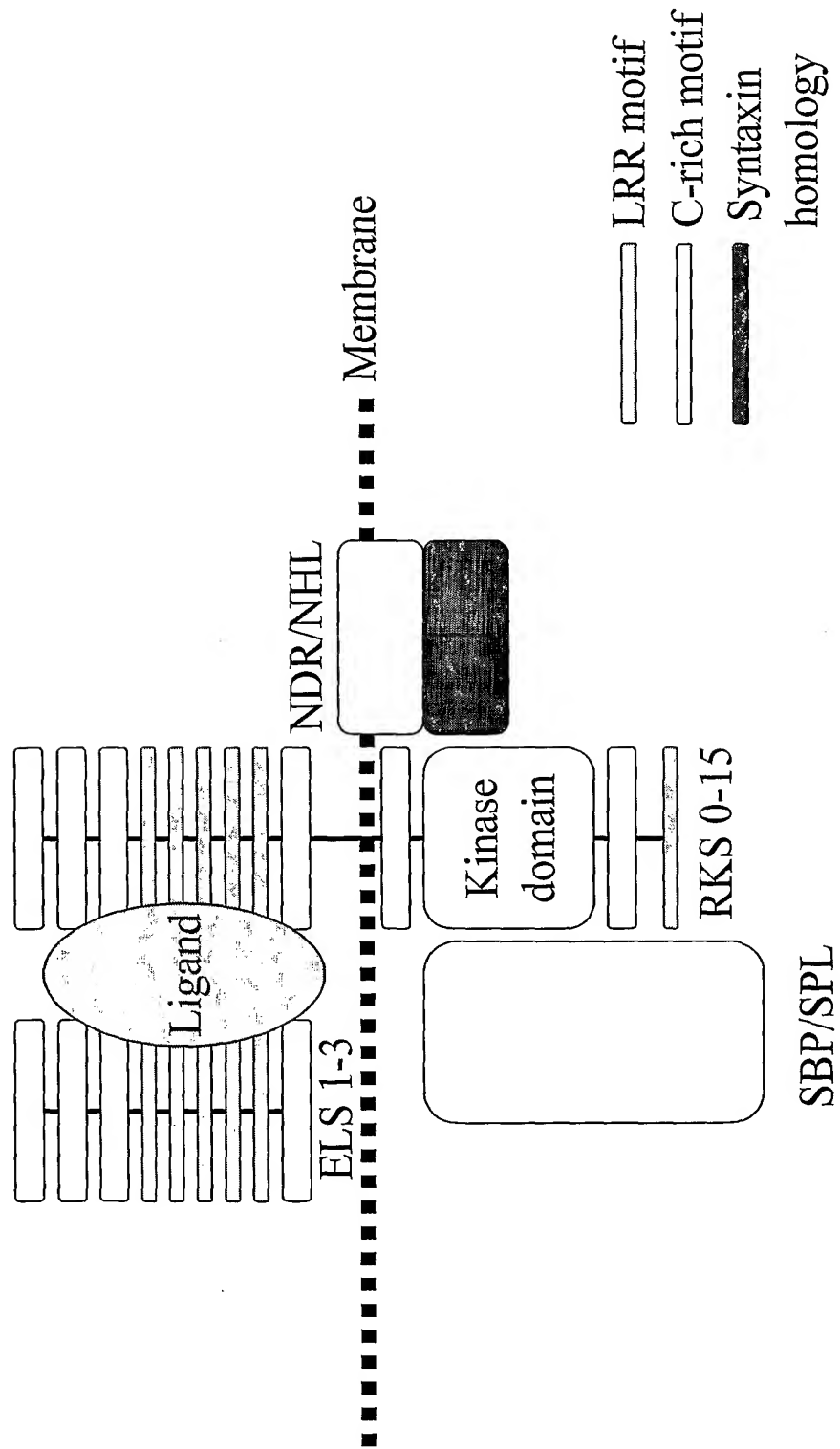
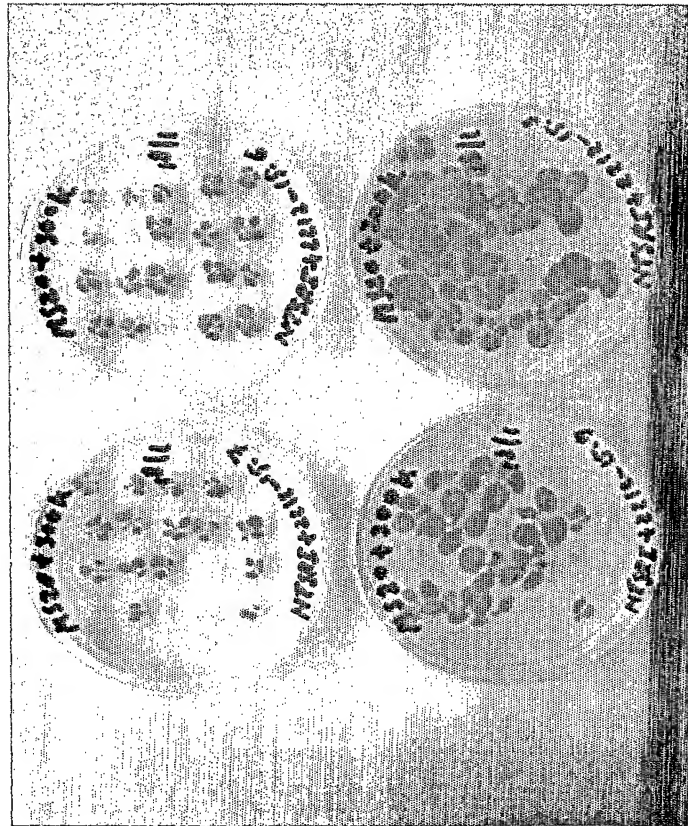


Fig. 5

GT-RKS4 determines seedling size
in *Nicotiana tabacum*.



Modifications in the
expression profile
of GT-RKS4 modulates
organ size within seedlings
of *Nicotiana tabacum*.

Fig. 7

GT-RKS4 determines organ size
in *Nicotiana tabacum*.

GT-RKS4-7S-T2

GT-RKS4-6S-T2

GT-RKS4-3S-T2

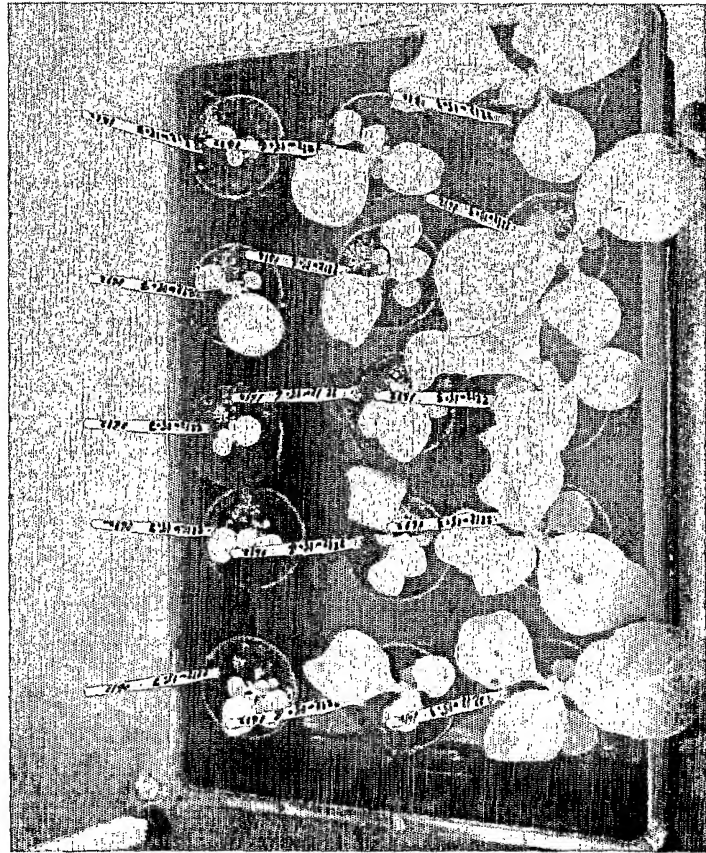
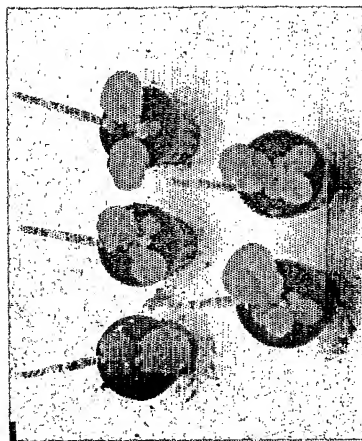
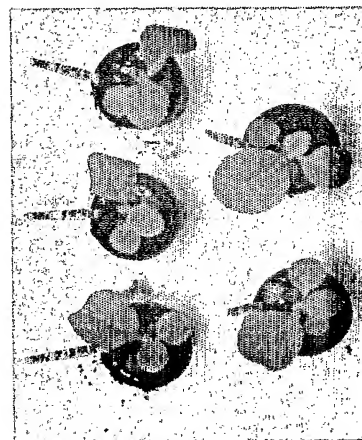


Fig. 8

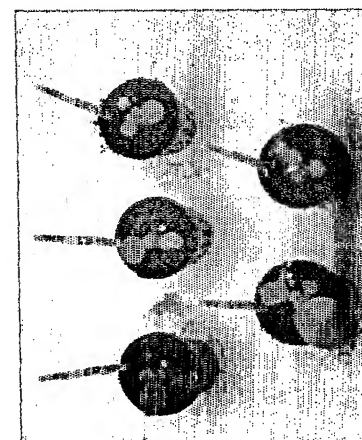
GT-RKS4 determines plant size
in *Nicotiana tabacum*



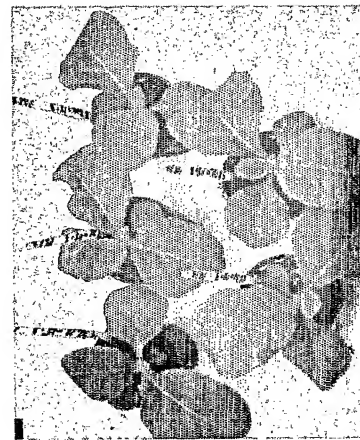
Empty vector control



GT-RKS4-15S-6T2



GT-RKS4-15S-7T2



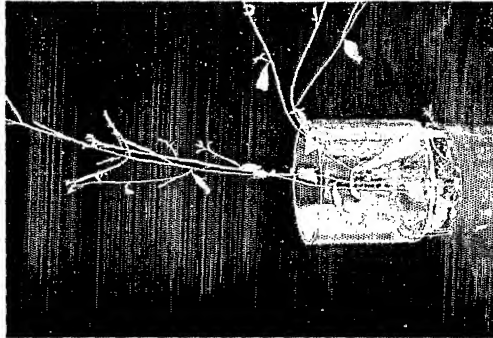
GT-RKS4-15S-3T2



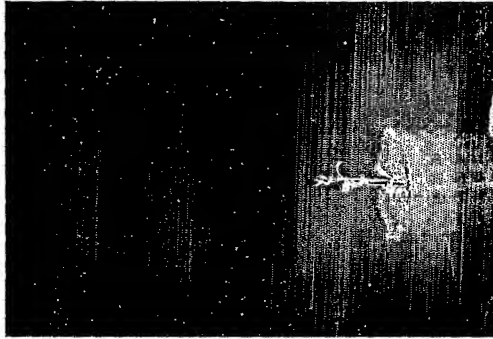
GT-RKS4-15S-9T2

Stable transformed GT-RKS4-antisense
in *Arabidopsis thaliana*

Wildtype WS



GT-RKS4-16a

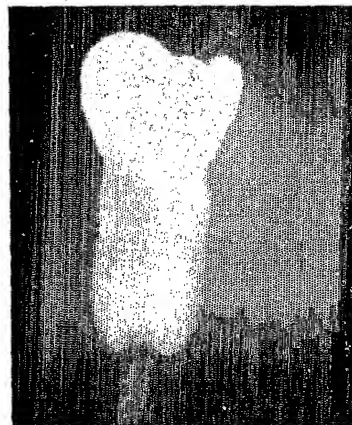


Overexpression of antisense GT-RKS4-1a
reduces plant and organ size.

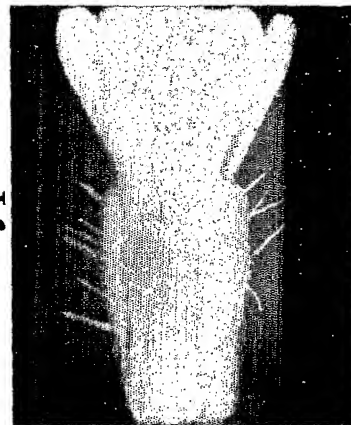
Fig. 9

Fig. 10

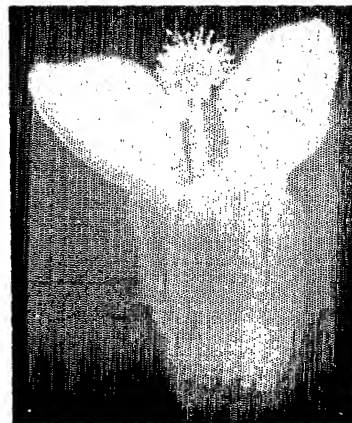
Ectopic expression of RKS4 and GAS3
gene products both result in increases
flower size in *Arabidopsis thaliana* WS



Wildtype WS



e35S::GAS3 sense



e35S::RKS4 sense

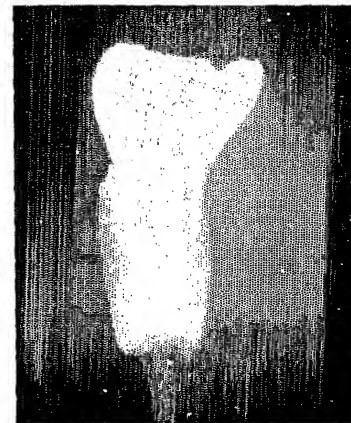
e35S::RKS4
antisense

Fig. 11

Ectopic expression of RKS4 in seedlings results
in the formation of meristematic regions in the
hypocotyl of *Arabidopsis thaliana* WS

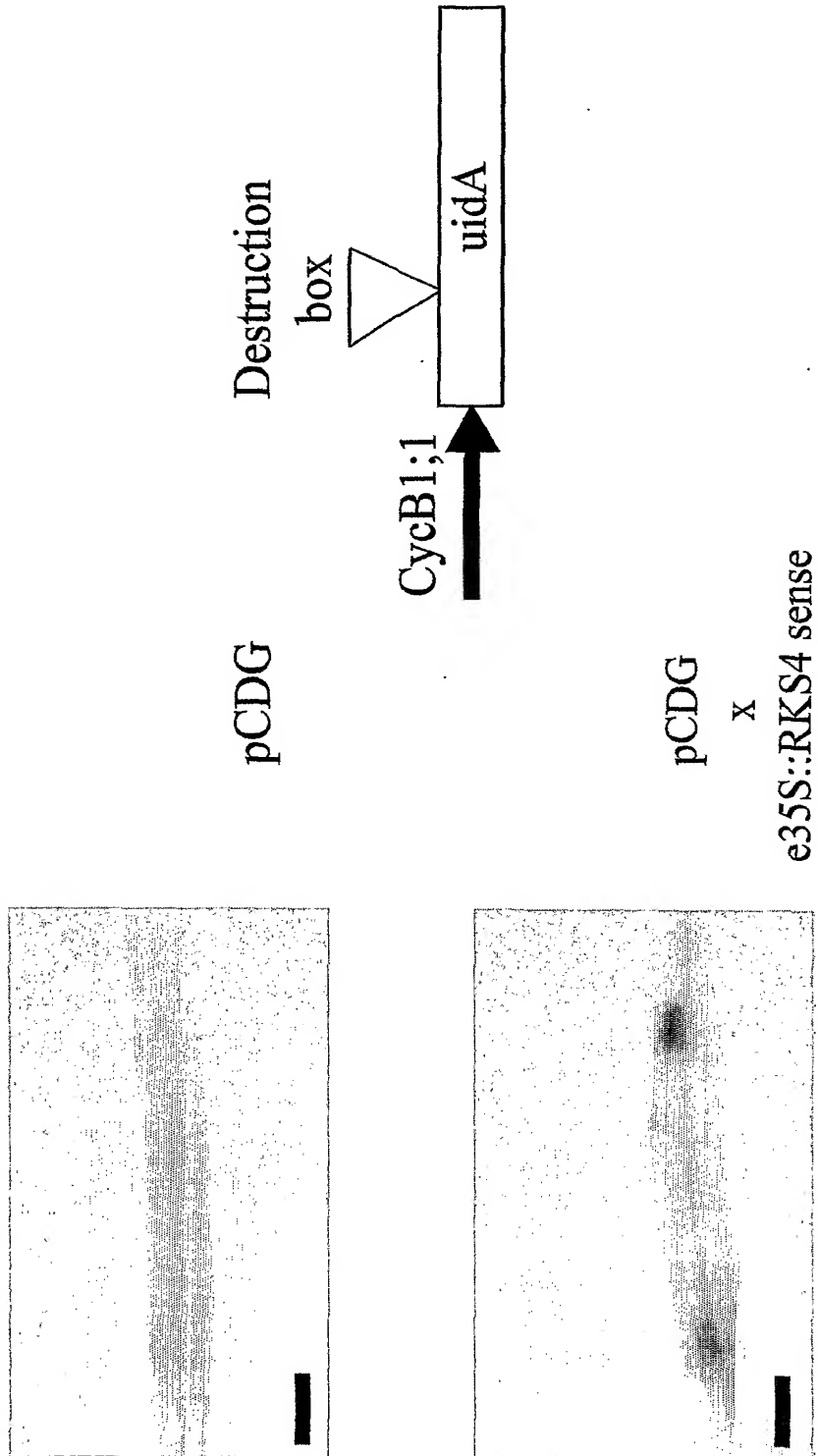


Fig. 12

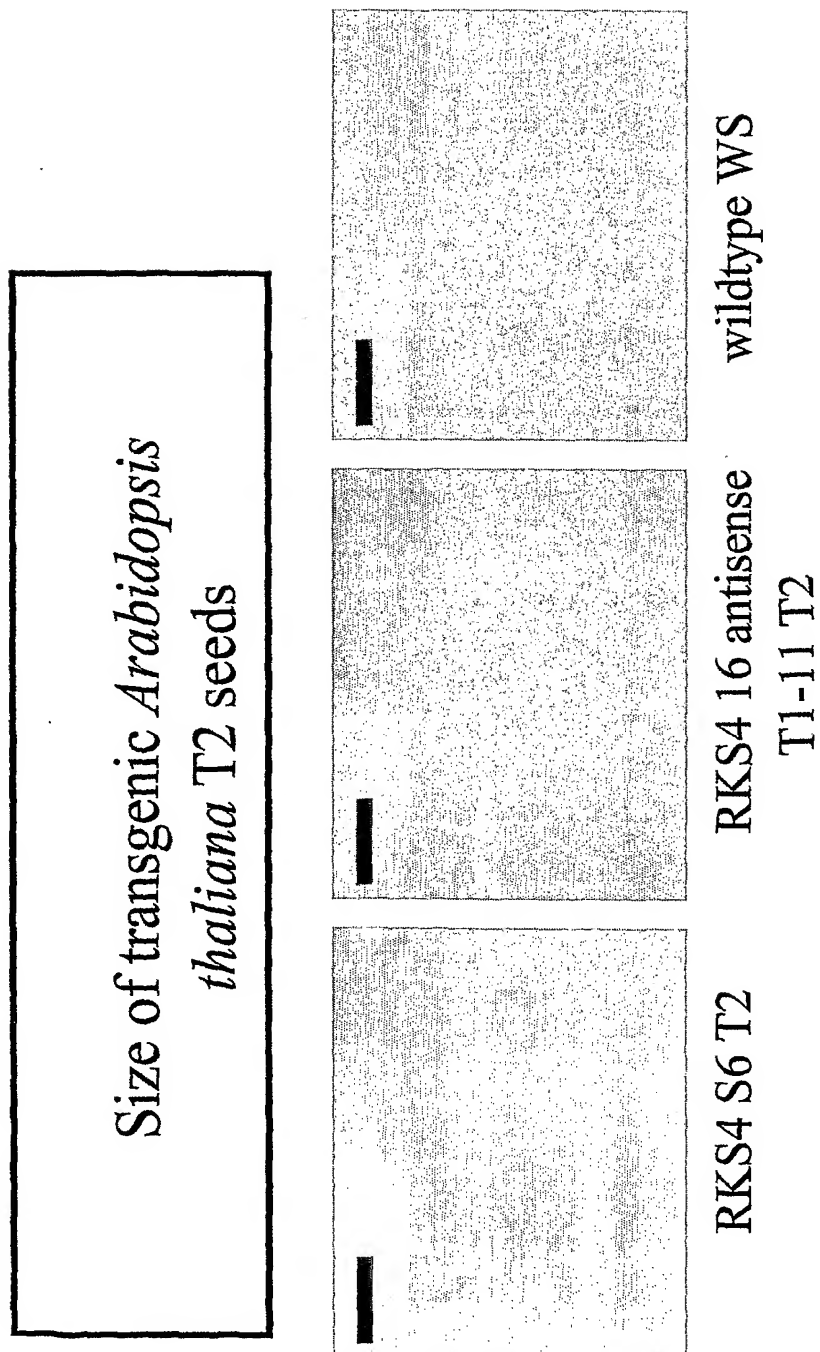


Fig. 13

RKS4 regulates cell number and cell size in *Arabidopsis thaliana*.

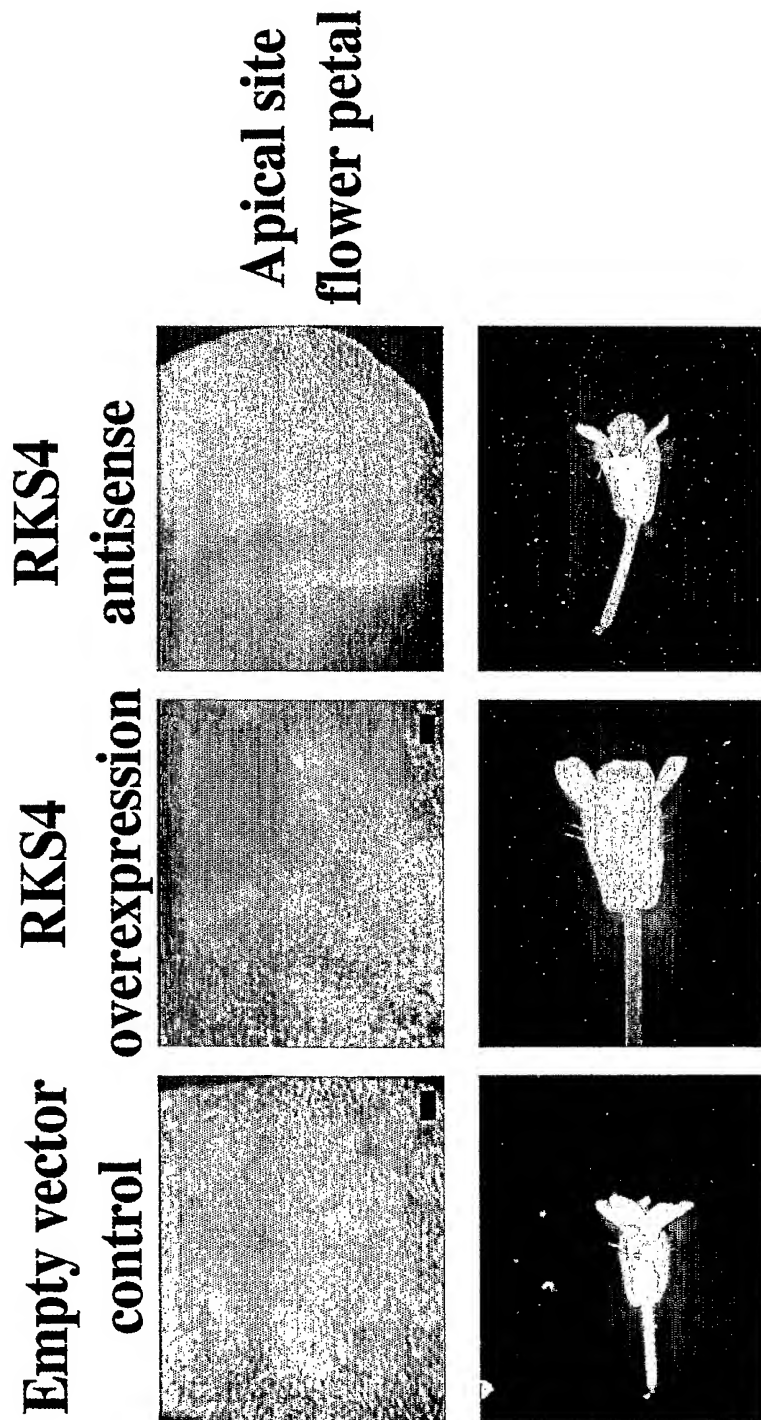


Fig. 14

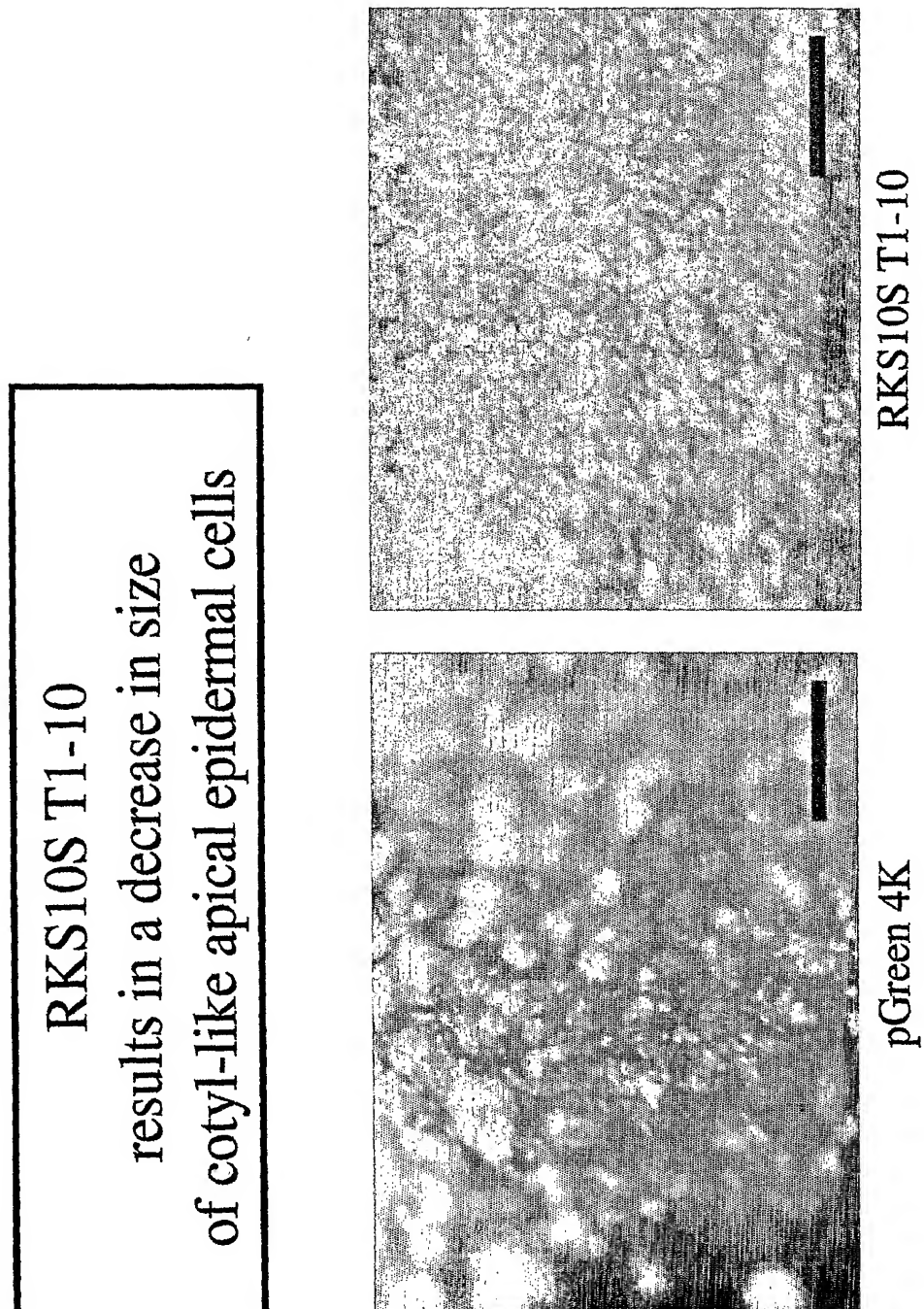


Fig. 15

RKS10antisense T1-4
results in an increase in size
of the cotyl epidermal cells

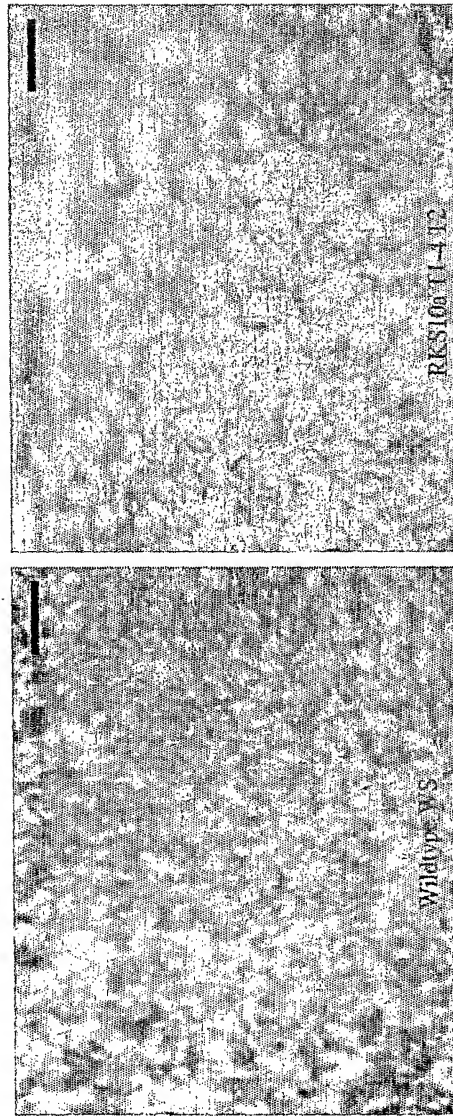


Fig. 16

Flower development from the same
inflorescence in transgenic
Arabidopsis thaliana

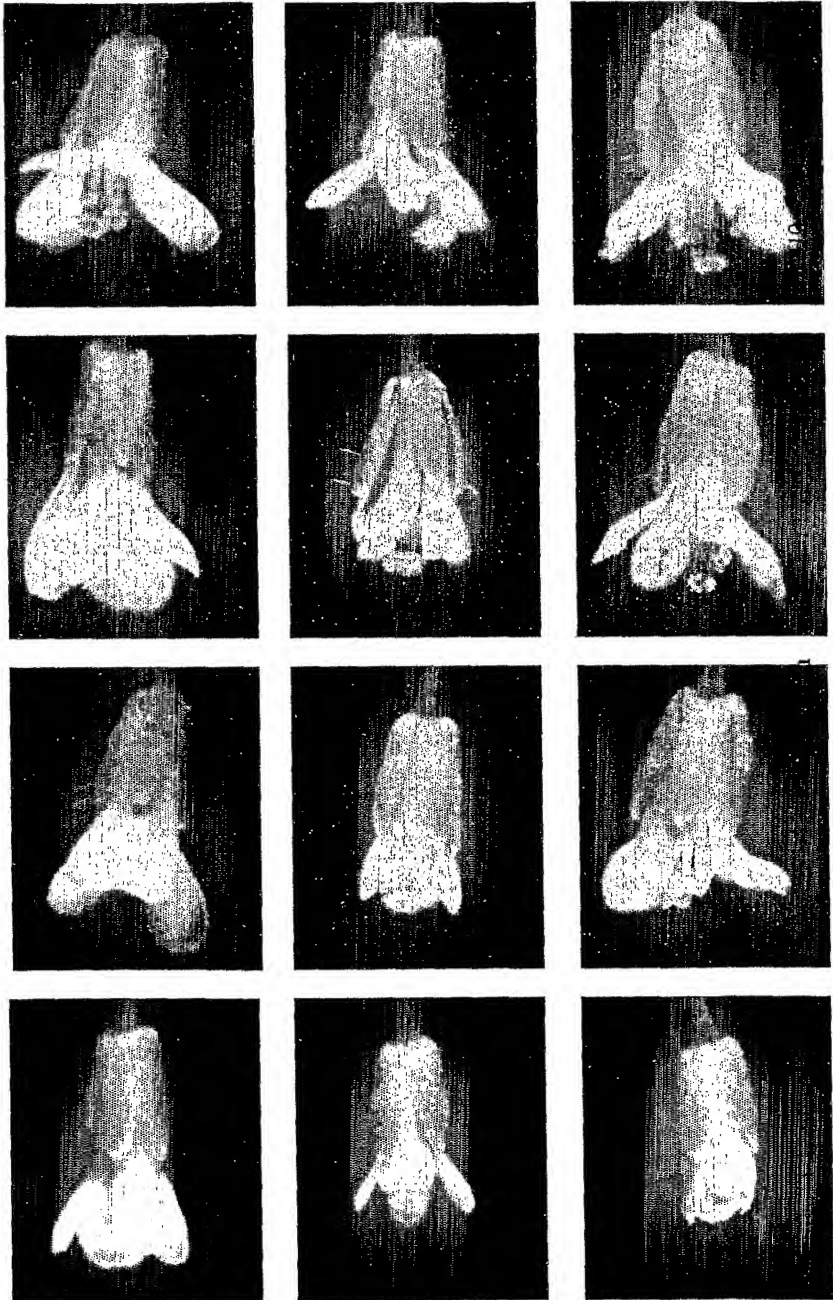


Fig. 17

Regeneration potential of
Arabidopsis transgenic seedlings.

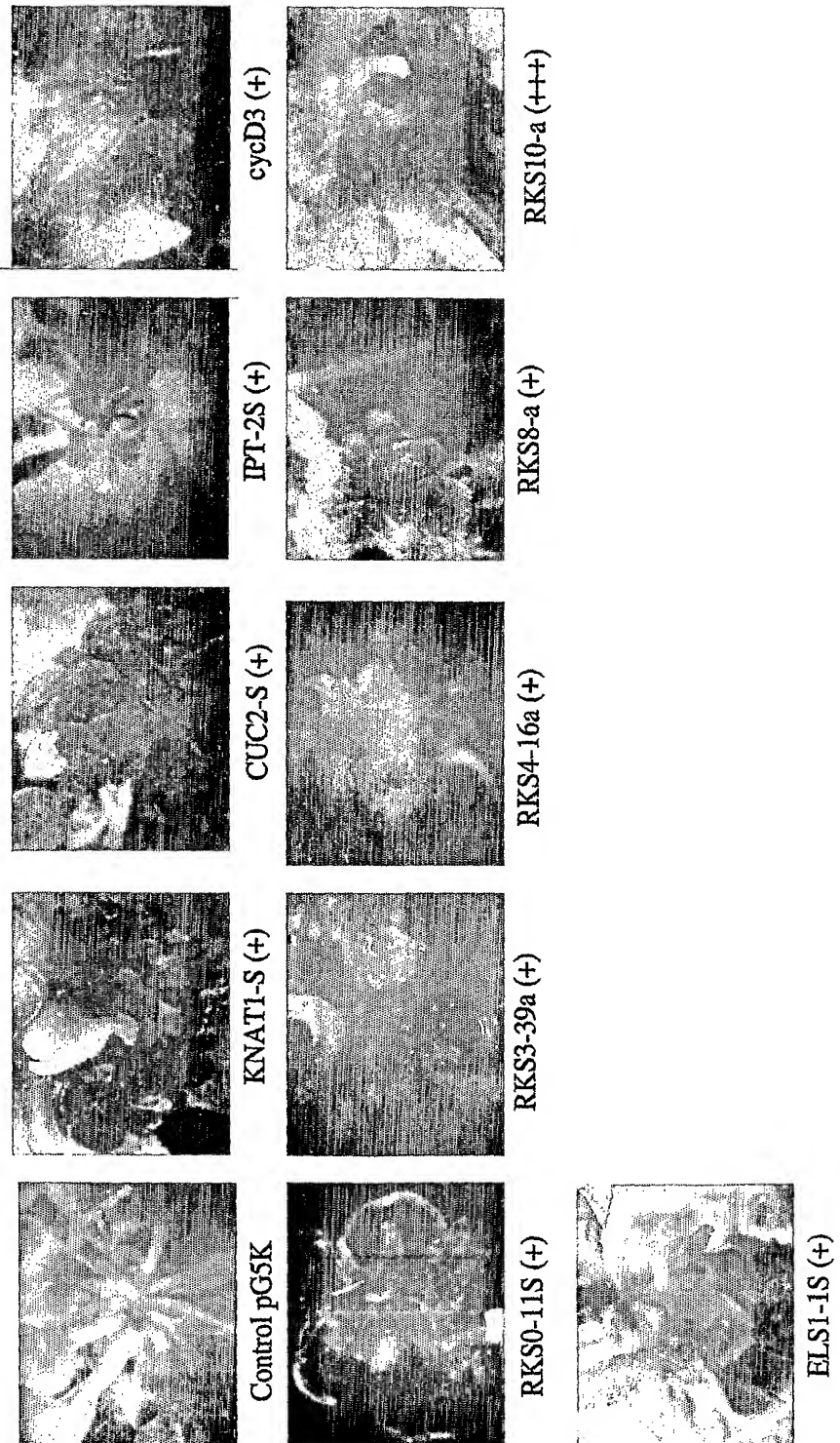


Fig. 18

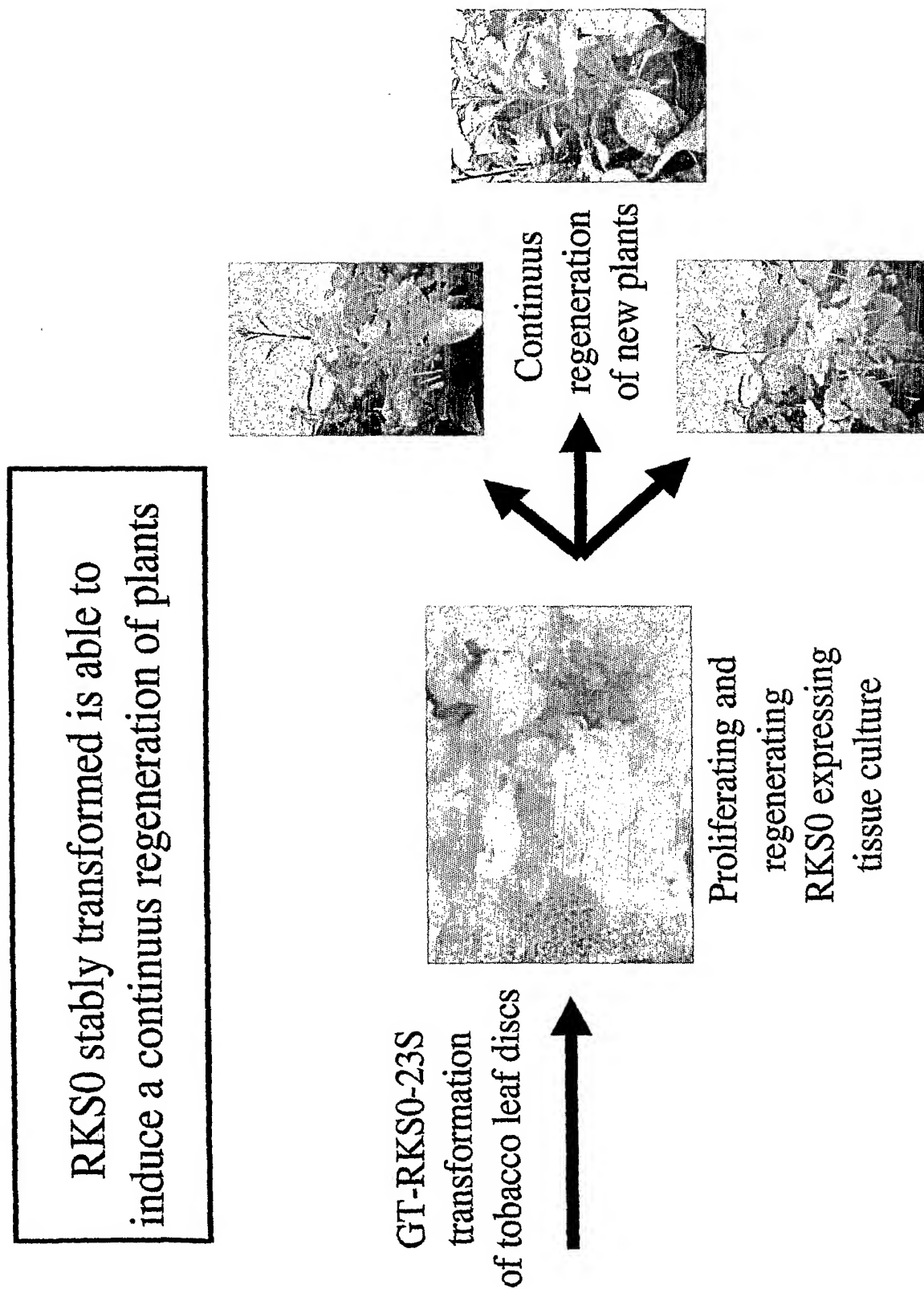


Fig. 19

Fasciation in transgenic
Arabidopsis thaliana

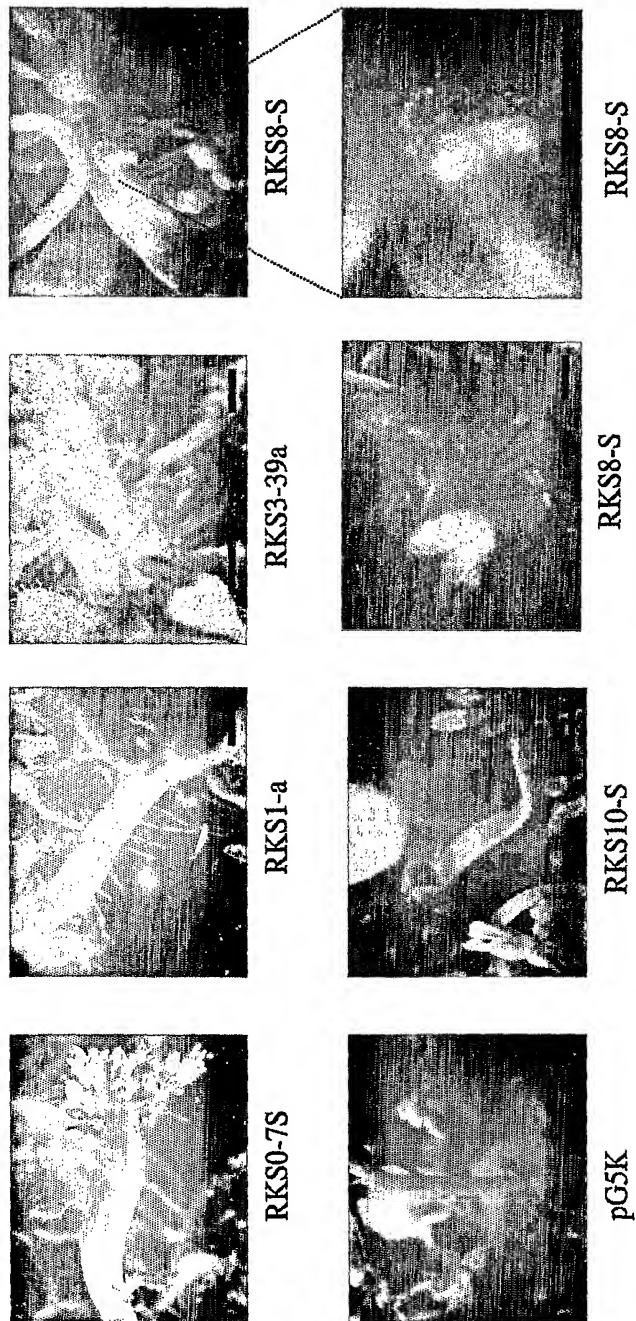


Fig. 20

Root growth of transgenic
Arabidopsis thaliana

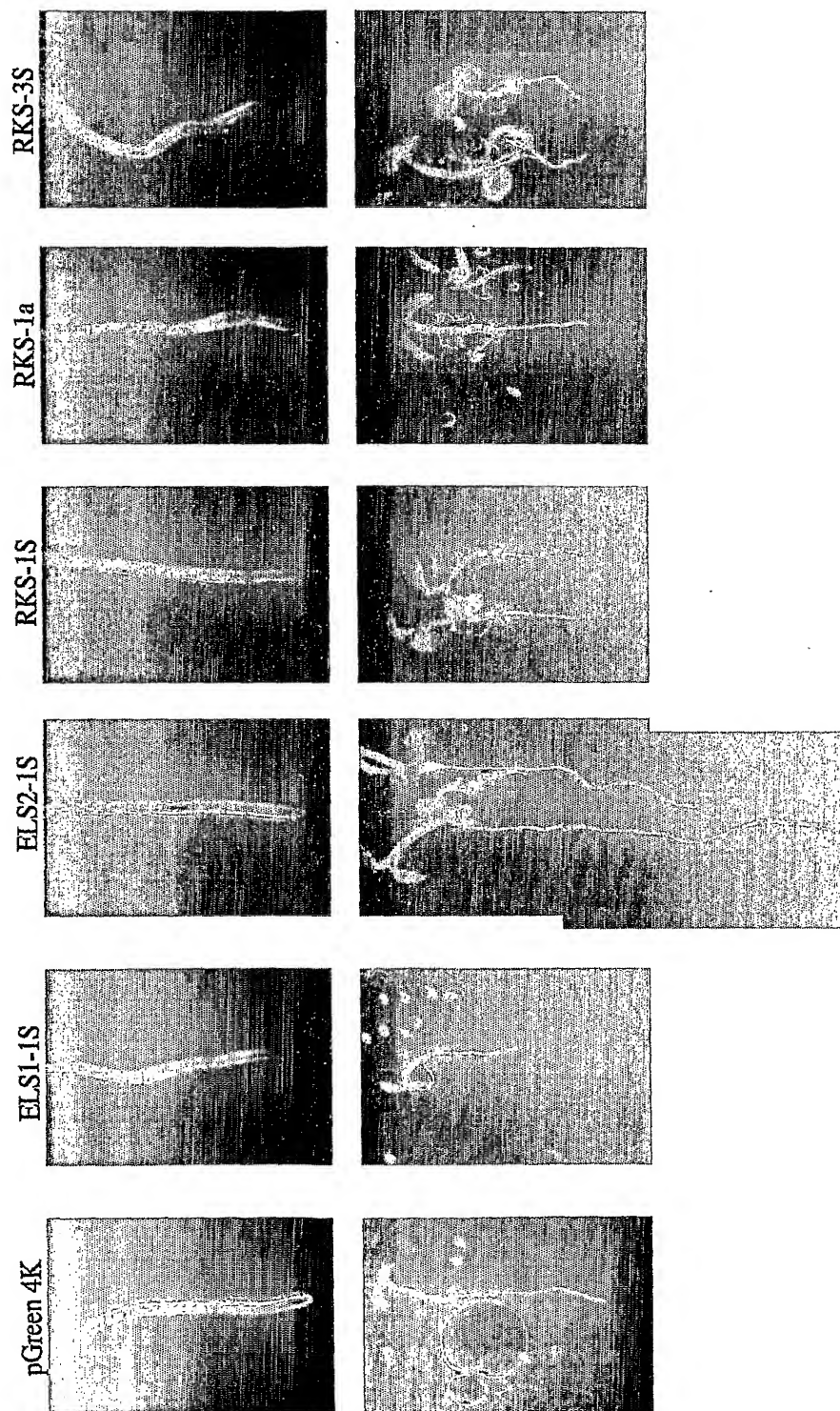


Fig. 21

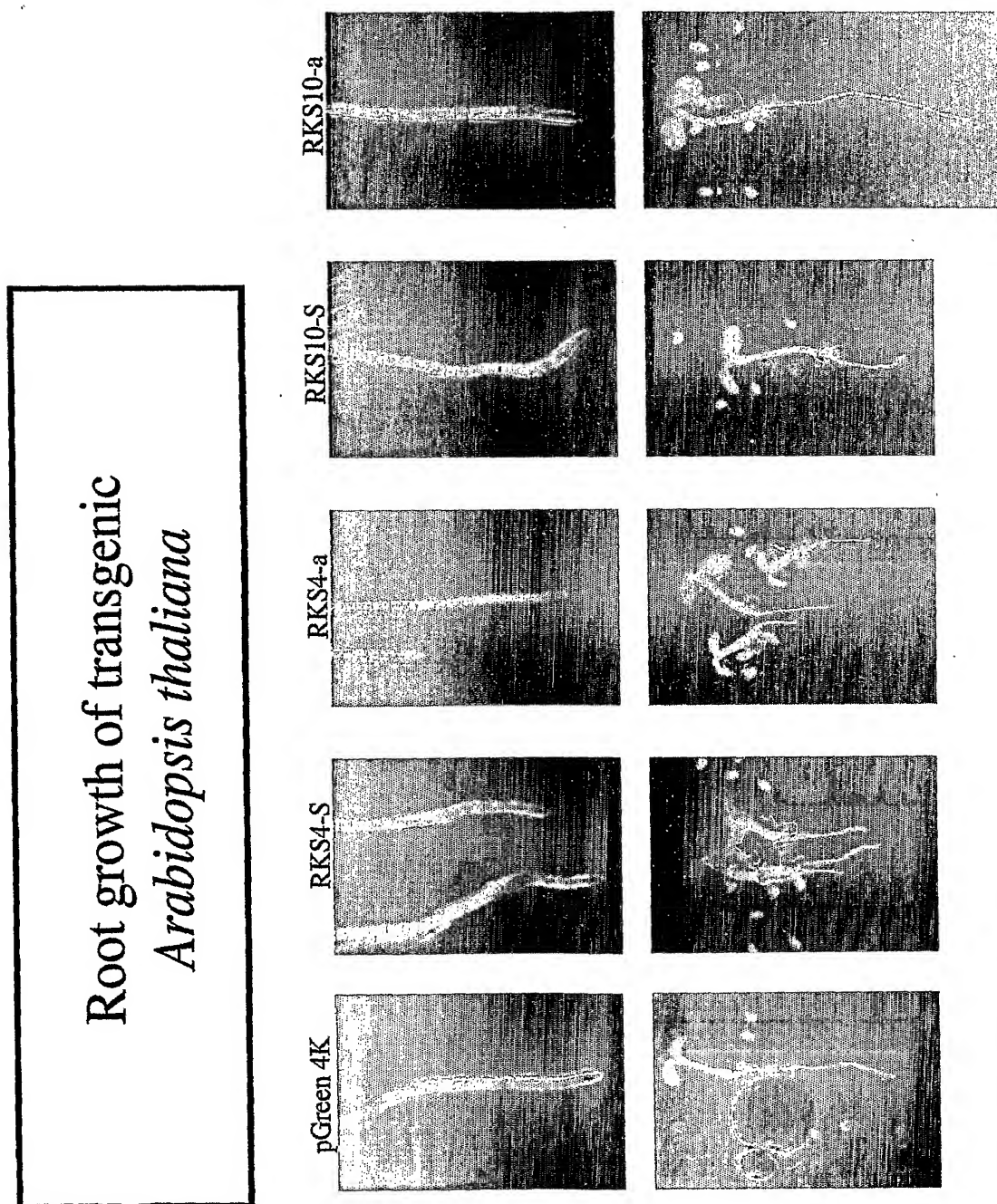


Fig. 22

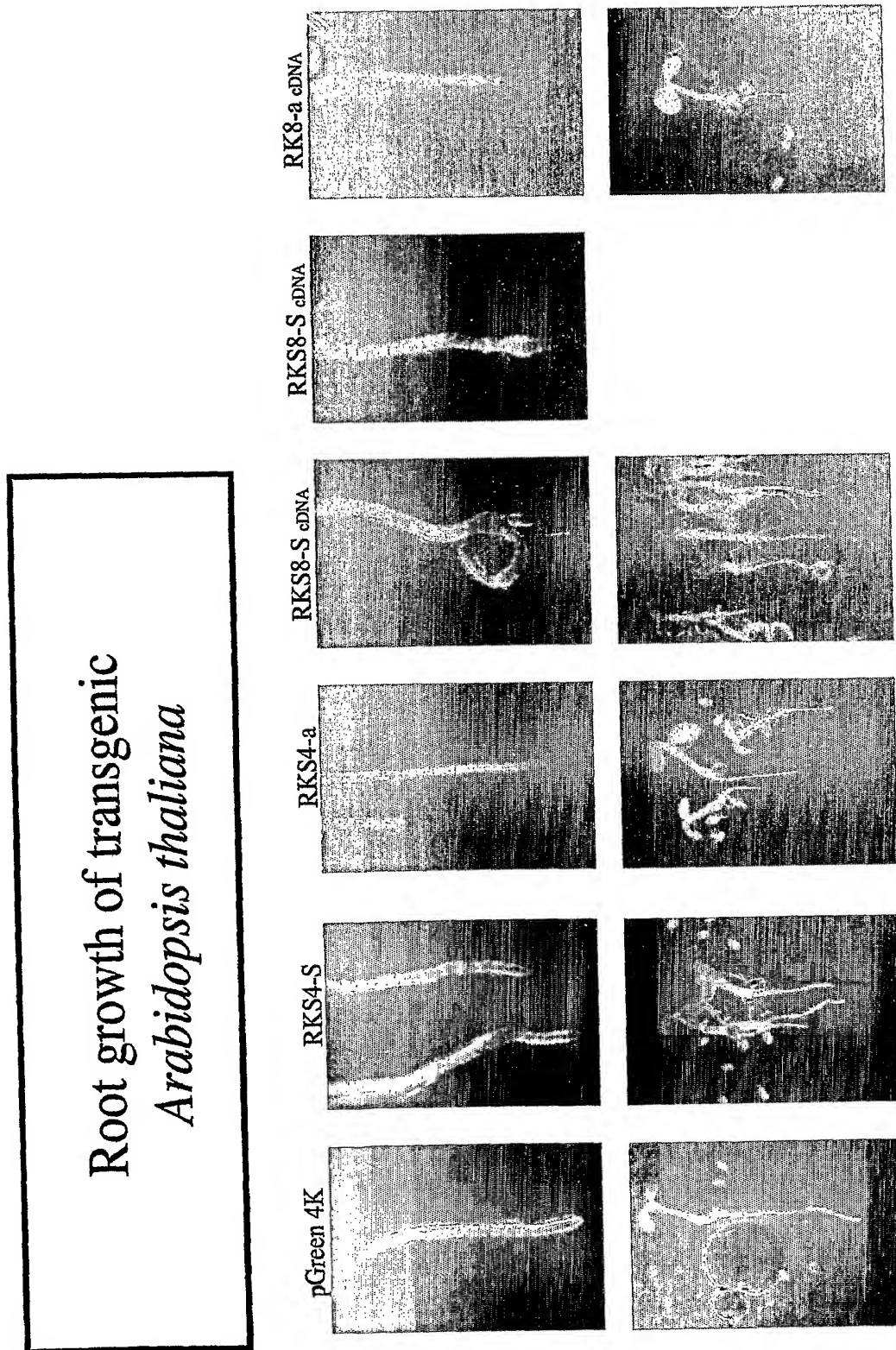


Fig. 23

Root growth of transgenic
Arabidopsis thaliana

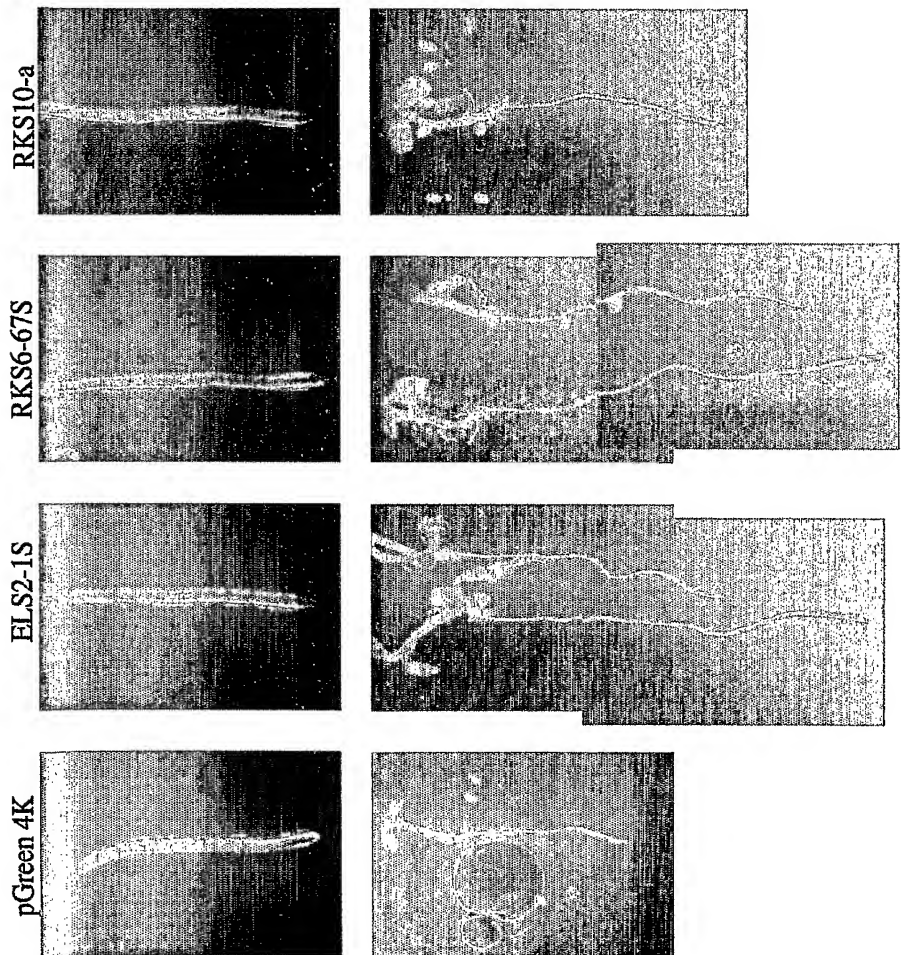


Fig. 24

Transgenic *Arabidopsis thaliana*
primary root length after 14 days
of germination

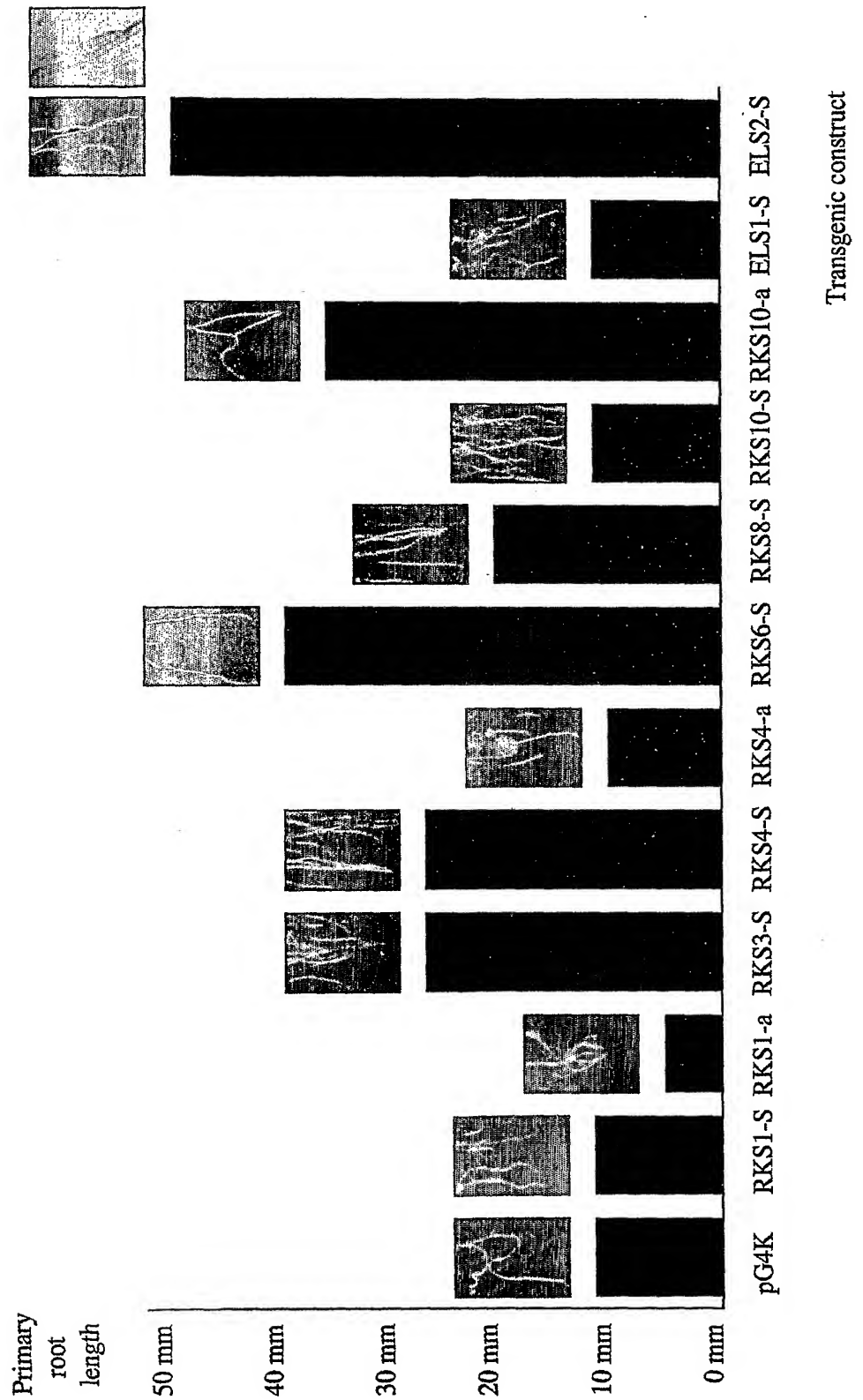


Fig. 25

Effects of RKS10 transgenic
constructs on plant development
of 45 days old *Arabidopsis* WS

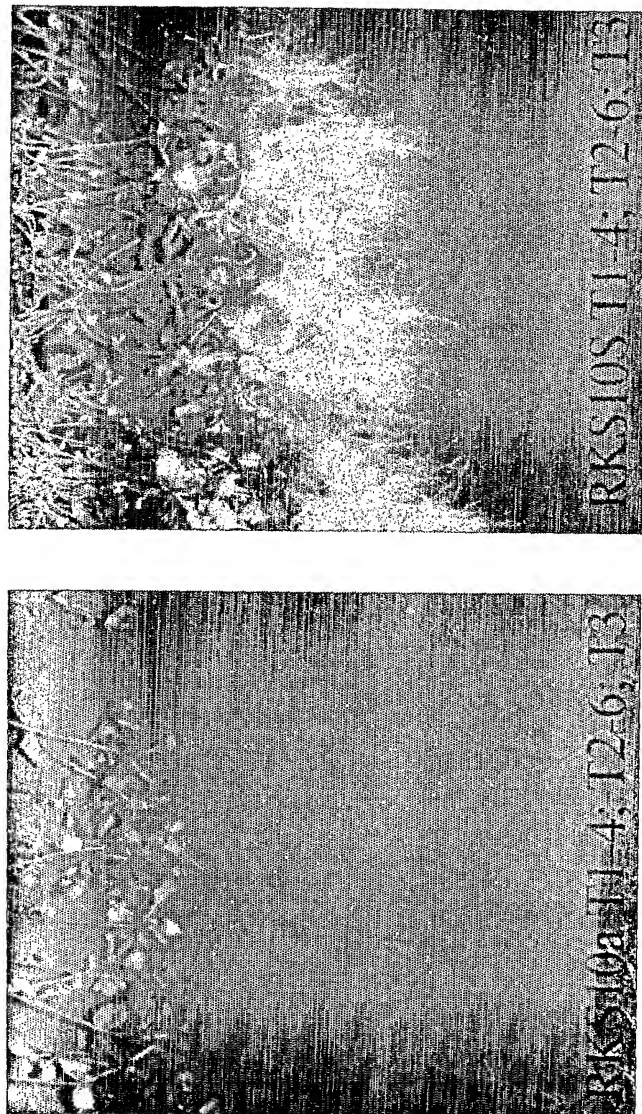


Fig. 26

Roots of Transgenic
Arabidopsis thaliana

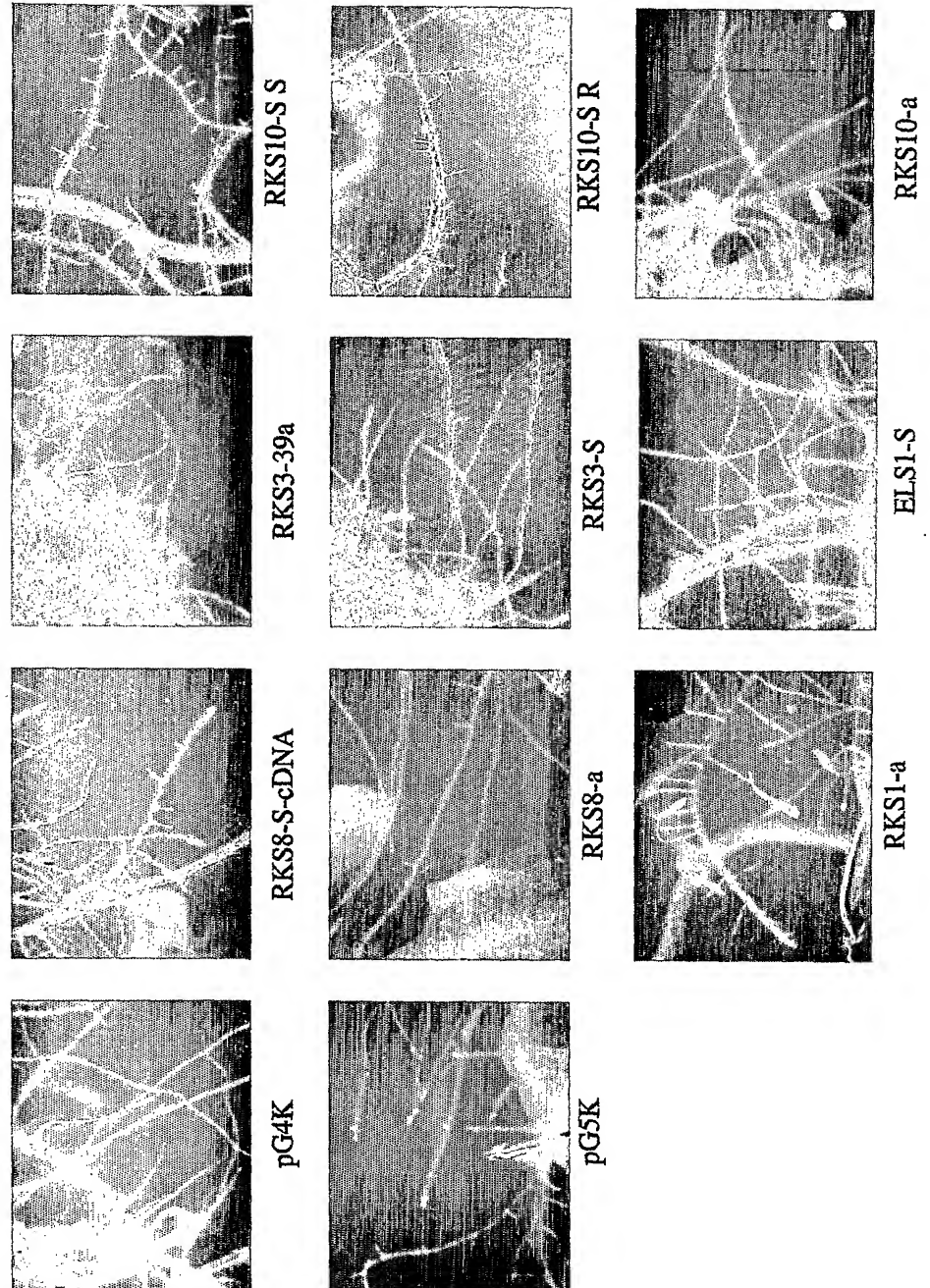


Fig. 27

Root cells of transgenic
Arabidopsis thaliana

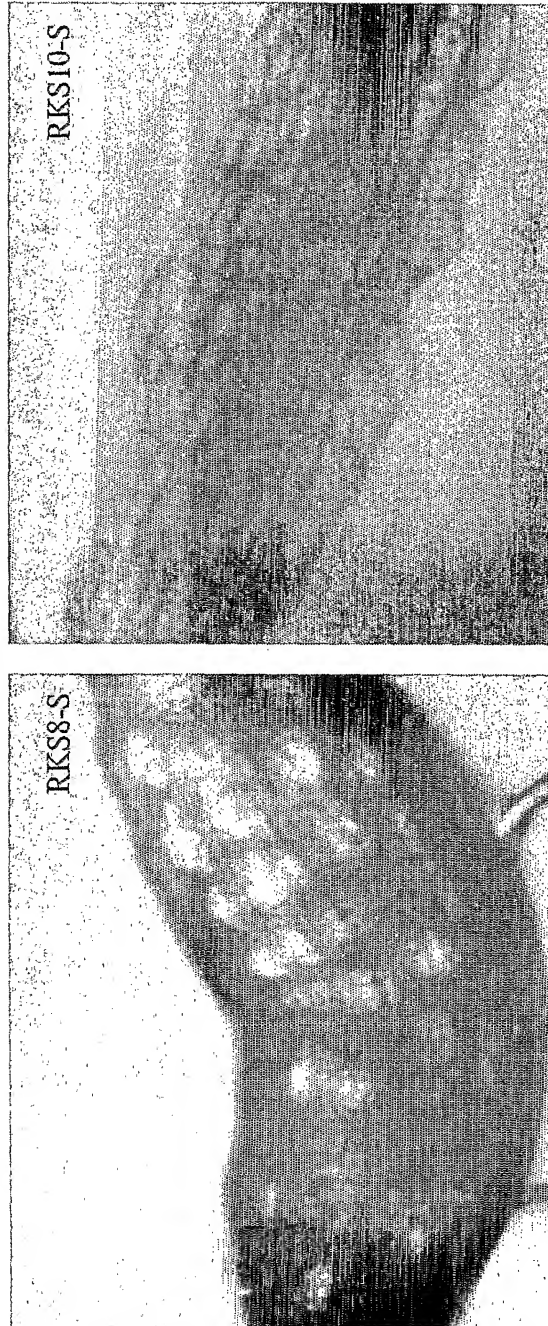


Fig. 28

Influences of T1 transgenic
Arabidopsis WS plants

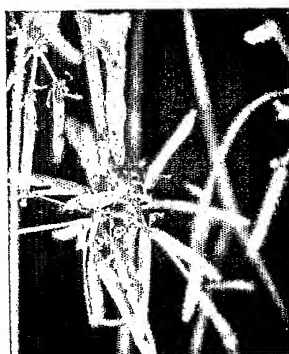
ELS-1-T1



RKS8-a-T1-10



RKS10-a-T2



RKS10-S-T1-10



Control pGreen4K

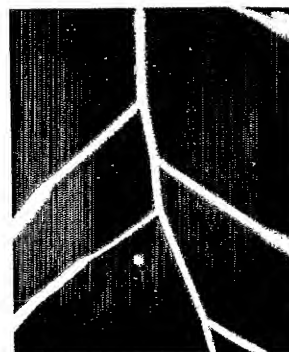


Fig. 29

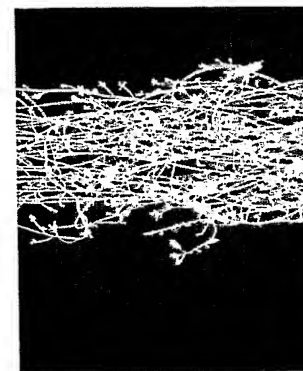
Influences of T1 transgenic
Arabidopsis WS plants



Control pG4K



RKS8-a-T1-10



RKS10-S-T1-10



Fig. 30

RKS10a T1 expression constructs in
Arabidopsis thaliana

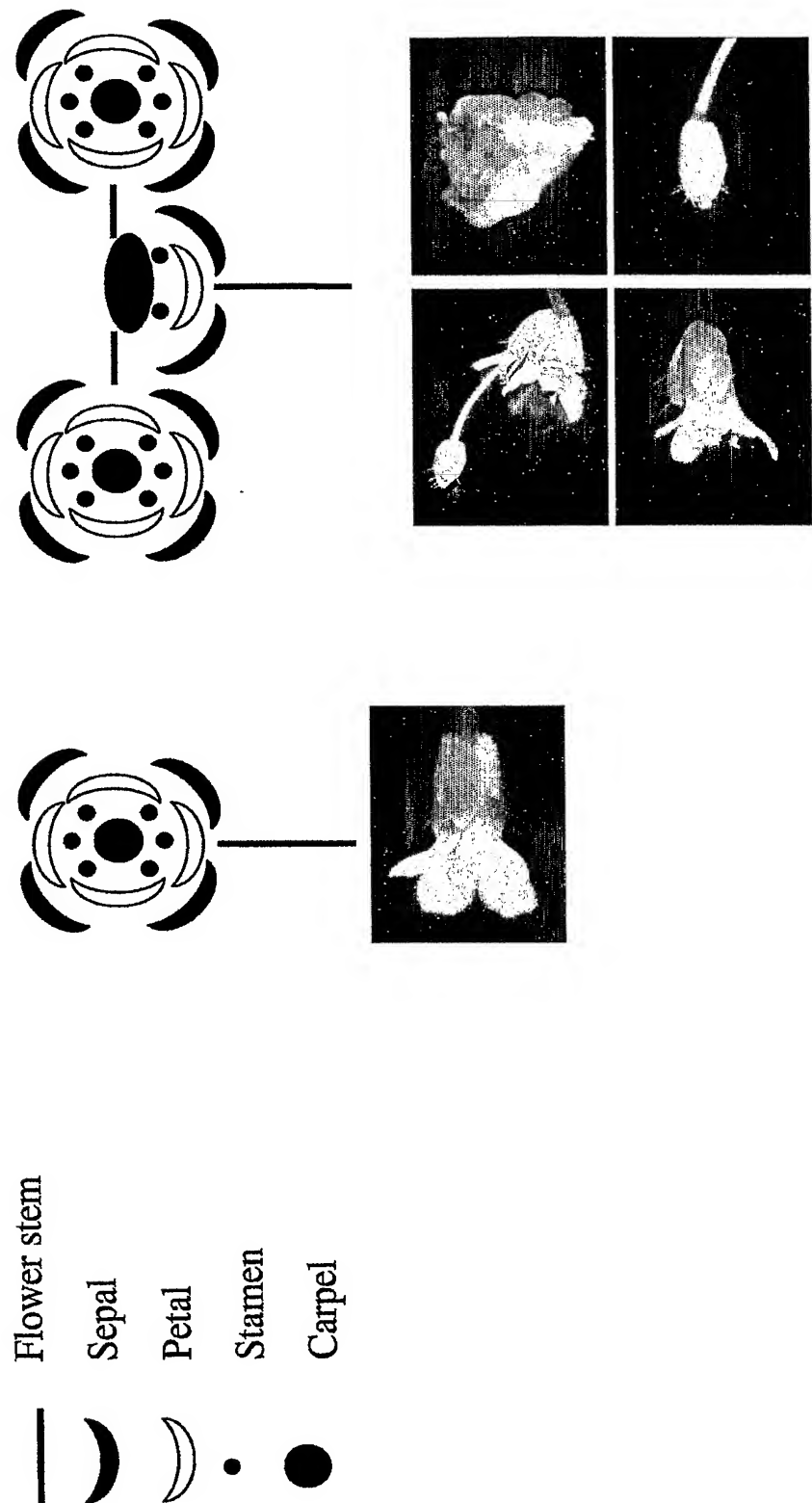
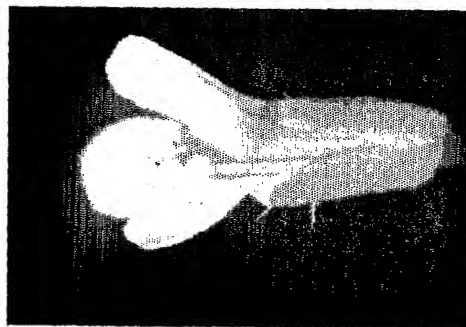
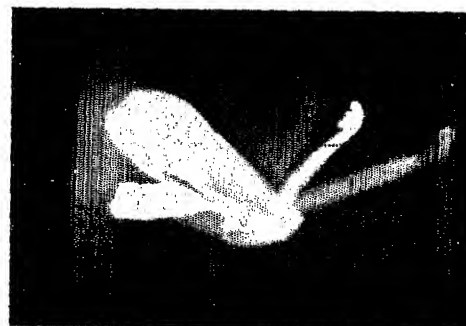


Fig. 32

RKS10 antisense effects in
Arabidopsis thaliana



pGreen 4K



RKS10a T1-11



detail flower RKS10a T1-11



Fig. 33

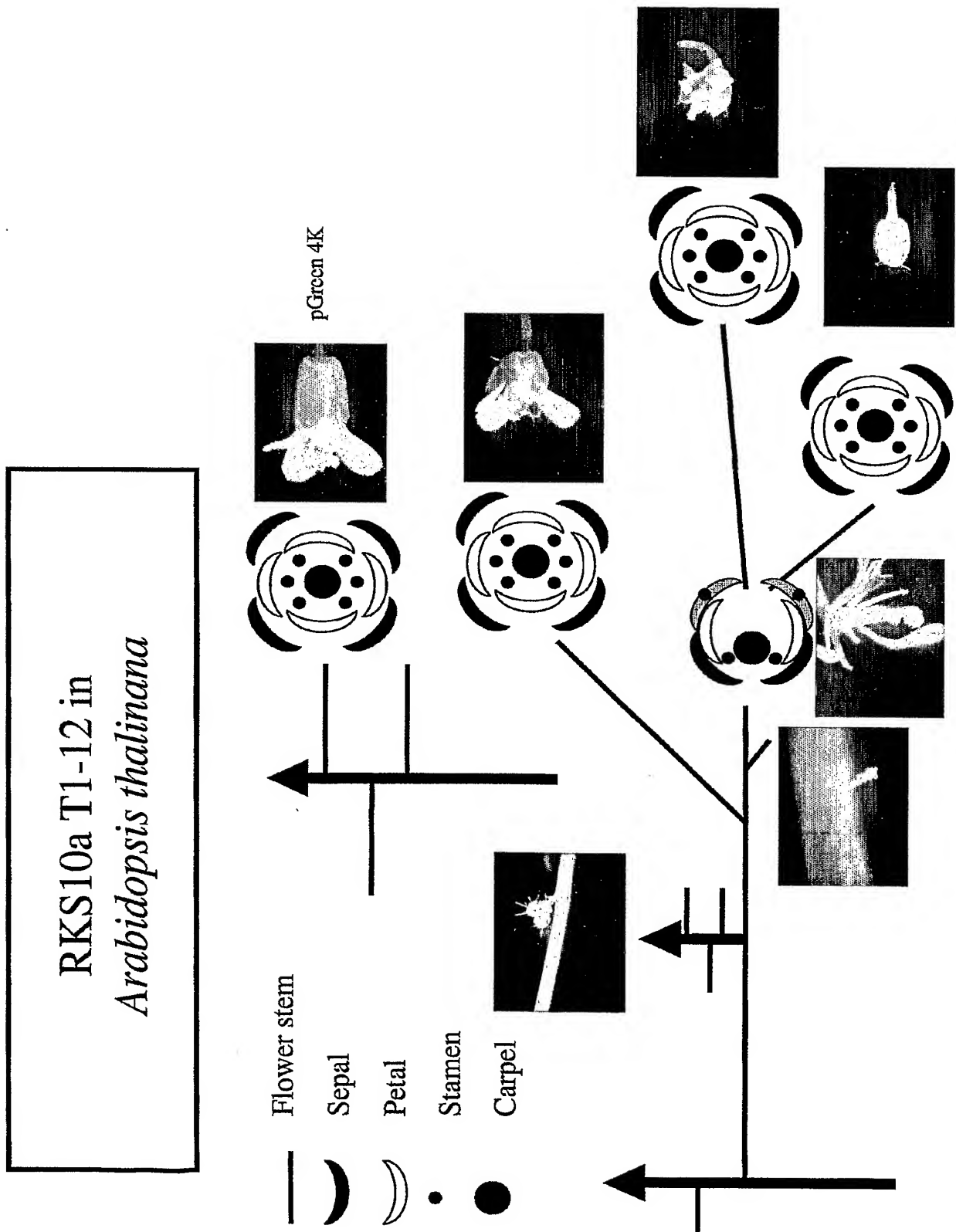


Fig. 34

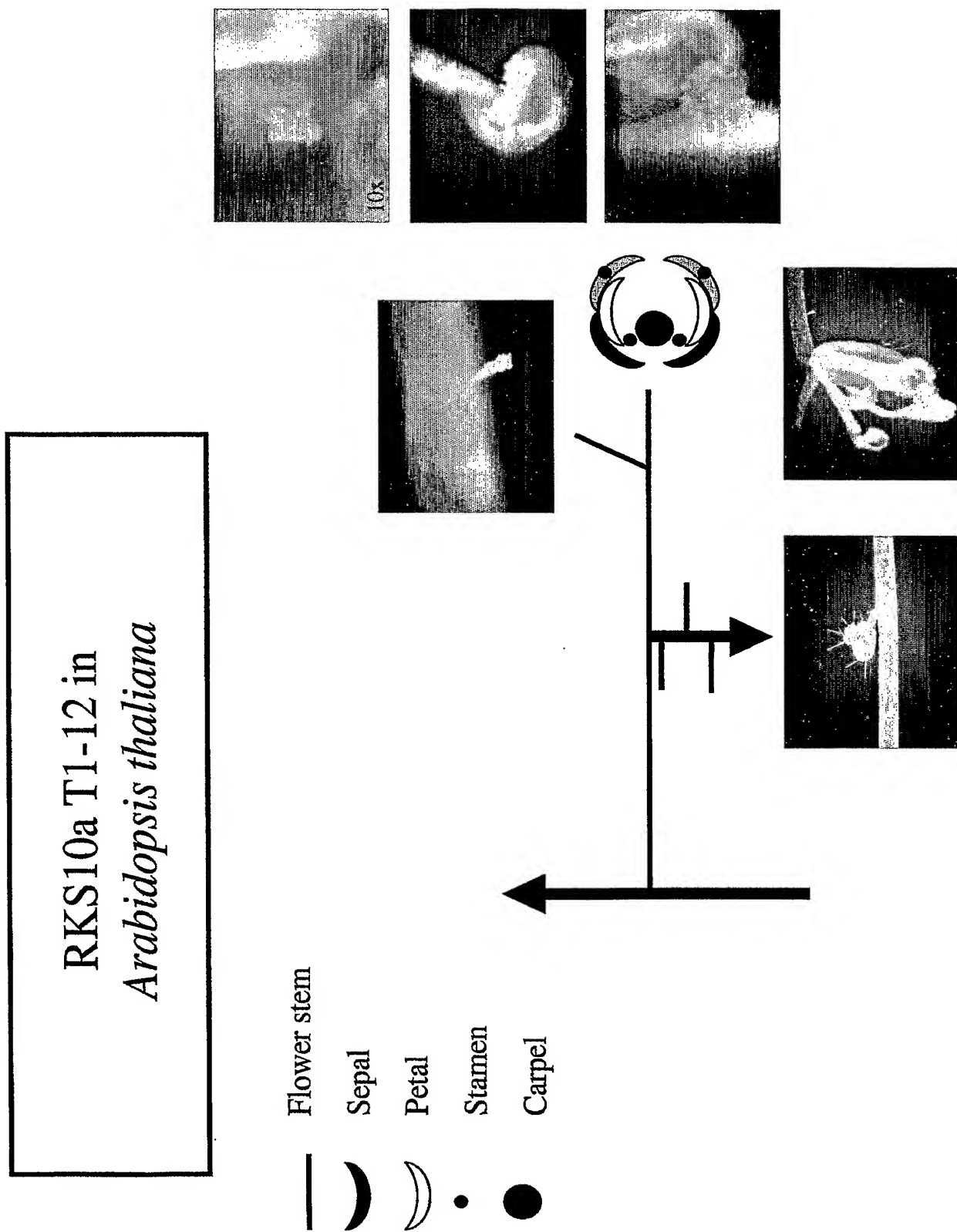


Fig. 35

RKS13 regulates
flower meristem identity in
Arabidopsis thaliana

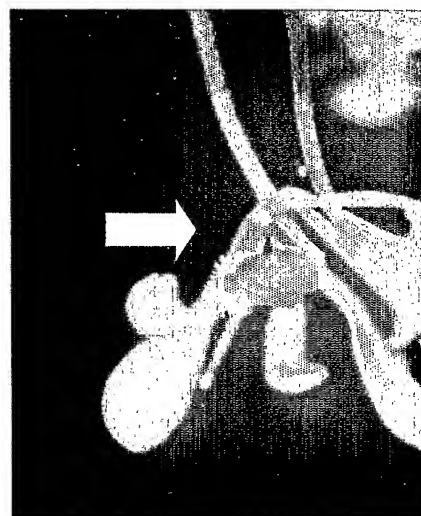
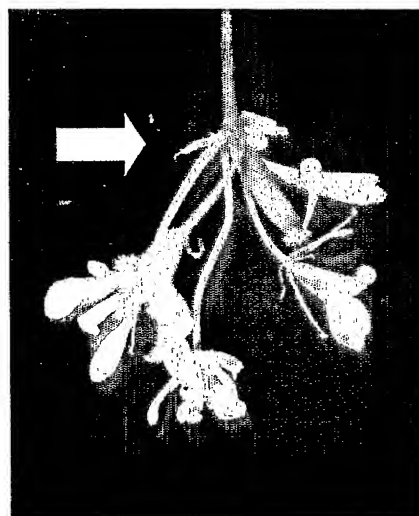
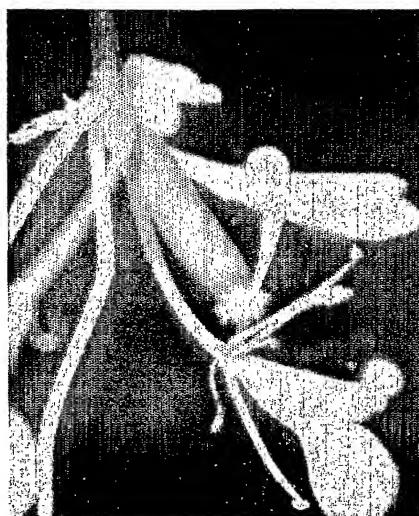


Fig. 36

Male sterile transgenes in
Arabidopsis thaliana

